

SEQUENCE LISTING

<110> Bryan, Bruce
Szent-Gyorgyi, Christopher
Szczepaniak, William

<120> RENILLA RENIFORMIS FLOUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE FLOUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIGH THROUGHPUT SCREENING AND NOVELTY ITEMS

<130> 24729-128

<140> Not Yet Assigned
<141> Herewith

<150> 60/189,691
<151> 2000-03-15

<150> 09/277,716
<151> 1999-03-26

<150> 08/757,046
<151> 1996-11-25

<150> 08/597,274
<151> 1996-02-06

<150> 08/908,909
<151> 1997-08-08

<150> 08/990,103
<151> 1997-12-12

<160> 33

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1196
<212> DNA
<213> Renilla

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<220>
<221> CDS
<222> (1)...(942)
<223> Renilla reniformis luciferase
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Ser Leu Lys Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg
1 5 10 15

48

```

atg ata act ggt ccg cag tgg tgg gcc aga tgt aaa caa atg aat gtt
Met Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val
          20           25           30

```

96

ctt gat tca ttt att aat tat tat gat tca gaa aaa cat gca gaa aat
 Leu Asp Ser Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn
 .
 35 40 45

144

```

gct gtt att ttt tta cat ggt aac gac gca tct tct tat tta tgg cga
Ala Val Ile Phe Leu His Glu Asn Ala Ala Ser Ser Tyr Leu Trp Arg
      50          55          60

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192

cat gtt gtg cca cat att gag cca gta gcg cggtt att ata cca gat His Val Val Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp 65 70 75 80	240
ctt att ggt atg ggc aaa tca ggc aaa tct ggt aat ggt tct tat agg Leu Ile Gly Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg 85 90 95	288
tta ctt gat cat tac aaa tat ctt act gca tgg ttg aac ttc tta att Leu Leu Asp His Tyr Lys Tyr Leu Thr Ala Trp Leu Asn Phe Leu Ile 100 105 110	336
tac caa aga aga tca ttt ttt gtc ggc cat gat tgg ggt gct tgg ttg Tyr Gln Arg Arg Ser Phe Phe Val Gly His Asp Trp Gly Ala Cys Leu 115 120 125	384
gca ttt cat tat agc tat gag cat caa gat aag atc aaa gca ata gtt Ala Phe His Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val 130 135 140	432
cac gct gaa agt gta gta gat gtg att gaa tca tgg gat gaa tgg cct His Ala Glu Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro 145 150 155 160	480
gat att gaa gaa gat att gcg ttg atc aaa tct gaa gaa gga gaa aaa Asp Ile Glu Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys 165 170 175	528
atg gtt ttg gag aat aac ttc ttc gtg gaa acc atg ttg cca tca aaa Met Val Leu Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys 180 185 190	576
atc atg aga aag tta gaa cca gaa gaa ttt gca gca tat ctt gaa cca Ile Met Arg Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro 195 200 205	624
ttc aaa gag aaa ggt gaa gtt cgt cgt cca aca tta tca tgg cct cgt Phe Lys Glu Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg 210 215 220	672
gaa atc ccg tta gta aaa ggt ggt aaa cct gac gtt gta caa att gtt Glu Ile Pro Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val 225 230 235 240	720
agg aat tat aat gct tat cta cgt gca agt gat gat tta cca aaa atg Arg Asn Tyr Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met 245 250 255	768
ttt att gaa tcg gat cca gga ttc ttt tcc aat gct att gtt gaa ggc Phe Ile Glu Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly 260 265 270	816
gcc aag aag ttt cct aat act gaa ttt gtc aaa gta aaa ggt ctt cat Ala Lys Lys Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His 275 280 285	864
ttt tcg caa gaa gat gca cct gat gaa atg gga aaa tat atc aaa tcg Phe Ser Gln Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser 290 295 300	912
ttc gtt gag cga gtt ctc aaa aat gaa caa taattacttt ggtttttat Phe Val Glu Arg Val Leu Lys Asn Glu Gln 305 310	962
ttacatttt cccgggtta ataataaaaa tgtcatttc aacaattta ttttaactga	1022

atatttcaca ggaaacattc atatatgtt attaatttag ctcgaactt actctgtcat	1082
atcattttgg aatattacct ctttcaatga aacttataa acagtggttc aattaattaa	1142
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<210> 2
<211> 1822
<212> DNA
<213> Cypridina hilagendorfii luciferase

<220>
<221> CDS
<222> (1)...(1665)
<223> Cypridina hilgendorfii luciferase

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1 5 10 15		
aac tgc cag gat gca tgt cct gta gaa gct gaa gca ccg tca agt aca	96	
Asn Cys Gln Asp Ala Cys Pro Val Glu Ala Glu Ala Pro Ser Ser Thr		
20 25 30		
cca aca gtc cca aca tct tgt gaa gct aaa gaa gga gaa tgt atc gat	144	
Pro Thr Val Pro Thr Ser Cys Glu Ala Lys Glu Gly Glu Cys Ile Asp		
35 40 45		
acc aga tgc gca aca tgt aaa cga gac ata cta tca gac gga ctg tgt	192	
Thr Arg Cys Ala Thr Cys Lys Arg Asp Ile Leu Ser Asp Gly Leu Cys		
50 55 60		
gaa aat aaa cca ggg aag aca tgc tgt aga atg tgc cag tat gta att	240	
Glu Asn Lys Pro Gly Lys Thr Cys Cys Arg Met Cys Gln Tyr Val Ile		
65 70 75 80		
gaa tcc aga gta gaa gct gct gga tat ttt aga acg ttt tac gcc aaa	288	
Glu Ser Arg Val Glu Ala Ala Gly Tyr Phe Arg Thr Phe Tyr Ala Lys		
85 90 95		
aga ttt aat ttt cag gaa cct ggt aaa tat gtg ctg gct cga gga acc	336	
Arg Phe Asn Phe Gln Glu Pro Gly Lys Tyr Val Leu Ala Arg Gly Thr		
100 105 110		
aag ggt ggc gac tgg tct gta acc ctc acc atg gag aat cta gat gga	384	
Lys Gly Gly Asp Trp Ser Val Thr Leu Thr Met Glu Asn Leu Asp Gly		
115 120 125		
cag aag gga gct gta ctg act aag aca aca ctg gag gta gta gga gac	432	
Gln Lys Gly Ala Val Leu Thr Lys Thr Leu Glu Val Val Gly Asp		
130 135 140		
gta ata gac att act caa gct act gca gat cct atc aca gtt aac gga	480	
Val Ile Asp Ile Thr Gln Ala Thr Ala Asp Pro Ile Thr Val Asn Gly		
145 150 155 160		
gga gct gac cca gtt atc gct aac ccg ttc aca att ggt gag gtg acc	528	
Gly Ala Asp Pro Val Ile Ala Asn Pro Phe Thr Ile Gly Glu Val Thr		
165 170 175		
att gct gtt gtc gaa ata ccc ggc ttc aat att aca gtc atc gaa ttc	576	
Ile Ala Val Val Glu Ile Pro Gly Phe Asn Ile Thr Val Ile Glu Phe		
180 185 190		

ttt aaa cta atc gtg ata gat att ctg gga gga aga tct gtg aga att Phe Lys Leu Ile Val Ile Asp Ile Leu Gly Gly Arg Ser Val Arg Ile 195 200 205	624
gct cca gac aca gca aac aaa gga ctg ata tct ggt atc tgt ggt aat Ala Pro Asp Thr Ala Asn Lys Gly Leu Ile Ser Gly Ile Cys Gly Asn 210 215 220	672
ctg gag atg aat gac gct gat gac ttt act aca gac gca gat cag ctg Leu Glu Met Asn Asp Ala Asp Asp Phe Thr Thr Asp Ala Asp Gln Leu 225 230 235 240	720
gcg atc caa ccc aac ata aac aaa gag ttc gac ggc tgc cca ttc tac Ala Ile Gln Pro Asn Ile Asn Lys Glu Phe Asp Gly Cys Pro Phe Tyr 245 250 255	768
ggg aat cct tct gat atc gaa tac tgc aaa ggt ctc atg gag cca tac Gly Asn Pro Ser Asp Ile Glu Tyr Cys Lys Gly Leu Met Glu Pro Tyr 260 265 270	816
aga gct gta tgt cgt aac aat atc aac ttc tac tat tac act ctg tcc Arg Ala Val Cys Arg Asn Asn Ile Asn Phe Tyr Tyr Thr Leu Ser 275 280 285	864
tgc gcc ttc gct tac tgt atg gga gga gaa gaa aga gct aaa cac gtc Cys Ala Phe Ala Tyr Cys Met Gly Gly Glu Arg Ala Lys His Val 290 295 300	912
ctt ttc gac tat gtt gag aca tgc gct gca ccg gaa acg aga gga acg Leu Phe Asp Tyr Val Glu Thr Cys Ala Ala Pro Glu Thr Arg Gly Thr 305 310 315 320	960
tgt gtt tta tca gga cat act ttc tat gac aca ttc gac aaa gcc aga Cys Val Leu Ser Gly His Thr Phe Tyr Asp Thr Phe Asp Lys Ala Arg 325 330 335	1008
tat caa ttc cag ggc cca tgc aaa gag ctt ctg atg gcc gca gac tgt Tyr Gln Phe Gln Gly Pro Cys Lys Glu Leu Leu Met Ala Ala Asp Cys 340 345 350	1056
tac tgg aac aca tgg gat gta aag gtt tca cat aga gat gtt gag tca Tyr Trp Asn Thr Trp Asp Val Lys Val Ser His Arg Asp Val Glu Ser 355 360 365	1104
tac act gag gta gag aaa gta aca atc agg aaa cag tca act gta gta Tyr Thr Glu Val Glu Lys Val Thr Ile Arg Lys Gln Ser Thr Val Val 370 375 380	1152
gat ttg att gtg gat ggc aag cag gtc aag gtt gga gga gtg gat gta Asp Leu Ile Val Asp Gly Lys Gln Val Lys Val Gly Gly Val Asp Val 385 390 395 400	1200
tct atc ccg tac agt tct gag aac aca tcc ata tac tgg cag gat gga Ser Ile Pro Tyr Ser Ser Glu Asn Thr Ser Ile Tyr Trp Gln Asp Gly 405 410 415	1248
gac atc ctg acg acg gcc atc cta cct gaa gct ctt gtc gtt aag ttc Asp Ile Leu Thr Ala Ile Leu Pro Glu Ala Leu Val Val Lys Phe 420 425 430	1296
aac ttt aag cag ctc ctt gta gtt cat atc aga gat cca ttc gat gga Asn Phe Lys Gln Leu Leu Val Val His Ile Arg Asp Pro Phe Asp Gly 435 440 445	1344
aag aca tgc ggc ata tgt ggt aac tat aat caa gat tca act gat gat	1392

Lys Thr Cys Gly Ile Cys Gly Asn Tyr Asn Gln Asp Ser Thr Asp Asp			
450	455	460	
ttc ttt gac gca gaa gga gca tgc gct ctg acc ccc aat ccc cca gga			1440
Phe Phe Asp Ala Glu Gly Ala Cys Ala Leu Thr Pro Asn Pro Pro Gly			
465	470	475	480
tgt aca gag gag cag aaa cca gaa gct gag cga ctc tgc aat agt cta			1488
Cys Thr Glu Glu Gln Lys Pro Glu Ala Glu Arg Leu Cys Asn Ser Leu			
485	490	495	
ttt gat agt tct atc gac gag aaa tgt aat gtc tgc tac aag cct gac			1536
Phe Asp Ser Ser Ile Asp Glu Lys Cys Asn Val Cys Tyr Lys Pro Asp			
500	505	510	
cgt att gca cga tgt atg tac gag tat tgc ctg agg gga cag caa gga			1584
Arg Ile Ala Arg Cys Met Tyr Glu Tyr Cys Leu Arg Gly Gln Gln Gly			
515	520	525	
ttc tgt gac cat gct tgg gag ttc aaa aaa gaa tgc tac ata aag cat			1632
Phe Cys Asp His Ala Trp Glu Phe Lys Lys Glu Cys Tyr Ile Lys His			
530	535	540	
gga gac act cta gaa gta cca cct gaa tgc caa taaaatgaaca aagatacaga			1685
Gly Asp Thr Leu Glu Val Pro Pro Glu Cys Gln			
545	550	555	
agctaagact actacacgag aagataaaaag agaagctgta gttcttcaaa aacagtatat			1745
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aaaaaaaaaaaa aaaaaaaaaa			1822
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<213> Luciola cruciata			
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<222> (1)...(1644)			
<223> Luciola cruciata luciferase			
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1	5	10	15
ttt tac cct atc gaa gag gga tct gct gga aca caa tta cgc aaa tac			96
Phe Tyr Pro Ile Glu Glu Gly Ser Ala Gly Thr Gln Leu Arg Lys Tyr			
20	25	30	
atg gag cga tat gca aaa ctt ggc gca att gct ttt aca aat gca gtt			144
Met Glu Arg Tyr Ala Lys Leu Gly Ala Ile Ala Phe Thr Asn Ala Val			
35	40	45	
act ggt gtt gat tat tct tac gcc gaa tac ttg gag aaa tca tgt tgt			192
Thr Gly Val Asp Tyr Ser Tyr Ala Glu Tyr Leu Glu Lys Ser Cys Cys			
50	55	60	
cta gga aaa gct ttg caa aat tat ggt ttg gtt gat ggc aga att			240
Leu Gly Lys Ala Leu Gln Asn Tyr Gly Leu Val Val Asp Gly Arg Ile			
65	70	75	80
gcg tta tgc agt gaa aac tgt gaa gaa ttt ttt att cct gta ata gcc			288
Ala Leu Cys Ser Glu Asn Cys Glu Phe Phe Ile Pro Val Ile Ala			

85	90	95	
gga ctg ttt ata ggt gta ggt gtt gca ccc act aat gag att tac act Gly Leu Phe Ile Gly Val Gly Val Ala Pro Thr Asn Glu Ile Tyr Thr 100	105	110	336
tta cgt gaa ctg gtt cac agt tta ggt atc tct aaa cca aca att gta Leu Arg Glu Leu Val His Ser Leu Gly Ile Ser Lys Pro Thr Ile Val 115	120	125	384
ttt agt tct aaa aaa ggc tta gat aaa gtt ata aca gta cag aaa aca Phe Ser Ser Lys Lys Gly Leu Asp Lys Val Ile Thr Val Gln Lys Thr 130	135	140	432
gta act act att aaa acc att gtt ata cta gat agc aaa gtt gat tat Val Thr Thr Ile Lys Thr Ile Val Ile Leu Asp Ser Lys Val Asp Tyr 145	150	155	480
cga gga tat caa tgt ctg gac acc ttt ata aaa aga aac act cca cca Arg Gly Tyr Gln Cys Leu Asp Thr Phe Ile Lys Arg Asn Thr Pro Pro 165	170	175	528
ggt ttt caa gca tcc agt ttc aaa act gtg gaa gtt gac cgt aaa gaa Gly Phe Gln Ala Ser Ser Phe Lys Thr Val Glu Val Asp Arg Lys Glu 180	185	190	576
caa gtt gct ctt ata atg aac tct tcg ggt tct acc ggt ttg cca aaa Gln Val Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys 195	200	205	624
ggc gta caa ctt act cac gaa aat aca gtc act aga ttt tct cat gct Gly Val Gln Leu Thr His Glu Asn Thr Val Thr Arg Phe Ser His Ala 210	215	220	672
aga gat ccg att tat ggt aac caa gtt tca cca ggc acc gct gtt tta Arg Asp Pro Ile Tyr Gly Asn Gln Val Ser Pro Gly Thr Ala Val Leu 225	230	235	720
act gtc gtt cca ttc cat cat ggt ttt ggt atg ttc act act cta ggg Thr Val Val Pro Phe His His Gly Phe Met Phe Thr Thr Leu Gly 245	250	255	768
tat tta att tgt ggt ttt cgt gtt gta atg tta aca aaa ttc gat gaa Tyr Leu Ile Cys Gly Phe Arg Val Val Met Leu Thr Lys Phe Asp Glu 260	265	270	816
gaa aca ttt tta aaa act cta caa gat tat aaa tgt aca agt gtt att Glu Thr Phe Leu Lys Thr Leu Gln Asp Tyr Lys Cys Thr Ser Val Ile 275	280	285	864
ctt gta ccg acc ttg ttt gca att ctc aac aaa agt gaa tta ctc aat Leu Val Pro Thr Leu Phe Ala Ile Leu Asn Lys Ser Glu Leu Leu Asn 290	295	300	912
aaa tac gat ttg tca aat tta gtt gag att gca tct ggc gga gca cct Lys Tyr Asp Leu Ser Asn Leu Val Glu Ile Ala Ser Gly Gly Ala Pro 305	310	315	960
tta tca aaa gaa gtt ggt gaa gct gtt gct aga cgc ttt aat ctt ccc Leu Ser Lys Glu Val Gly Glu Ala Val Ala Arg Arg Phe Asn Leu Pro 325	330	335	1008
ggt gtt cgt caa ggt tat ggt tta aca gaa aca aca tct gcc att att Gly Val Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Ile 340	345	350	1056

att aca cca gaa gga gac gat aaa cca gga gct tct gga aaa gtc gtg Ile Thr Pro Glu Gly Asp Asp Lys Pro Gly Ala Ser Gly Lys Val Val 355 360 365	1104
ccg ttg ttt aaa gca aaa gtt att gat ctt gat acc aaa aaa tct tta Pro Leu Phe Lys Ala Lys Val Ile Asp Leu Asp Thr Lys Lys Ser Leu 370 375 380	1152
ggc cct aac aga cgt gga gaa gtt tgc ttt aaa gga cct atg ctt atg Gly Pro Asn Arg Arg Gly Glu Val Cys Val Lys Gly Pro Met Leu Met 385 390 395 400	1200
aaa ggt tat gta aat aat cca gaa gca aca aaa gaa ctt att gac gaa Lys Gly Tyr Val Asn Asn Pro Glu Ala Thr Lys Glu Leu Ile Asp Glu 405 410 415	1248
gaa ggt tgg ctg cac acc gga gat att gga tat tat gat gaa gaa aaa Glu Gly Trp Leu His Thr Gly Asp Ile Gly Tyr Tyr Asp Glu Glu Lys 420 425 430	1296
cat ttc ttt att gtc gat cgt ttg aag tct tta atc aaa tac aaa gga His Phe Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly 435 440 445	1344
tac caa gta cca cct gcc gaa tta gaa tcc gtt ctt ttg caa cat cca Tyr Gln Val Pro Pro Ala Glu Leu Glu Ser Val Leu Leu Gln His Pro 450 455 460	1392
tct atc ttt gat gct ggt gtt gcc ggc gtt cct gat cct gta gct ggc Ser Ile Phe Asp Ala Gly Val Ala Gly Val Pro Asp Pro Val Ala Gly 465 470 475 480	1440
gag ctt cca gga gcc gtt gtt gta ctg gaa agc gga aaa aat atg acc Glu Leu Pro Gly Ala Val Val Val Leu Glu Ser Gly Lys Asn Met Thr 485 490 495	1488
gaa aaa gaa gta atg gat tat gtt gca agt caa gtt tca aat gca aaa Glu Lys Glu Val Met Asp Tyr Val Ala Ser Gln Val Ser Asn Ala Lys 500 505 510	1536
cgt tta cgt ggt ggt gtt cgt ttt gtg gat gaa gta cct aaa ggt ctt Arg Leu Arg Gly Gly Val Arg Phe Val Asp Glu Val Pro Lys Gly Leu 515 520 525	1584
act gga aaa att gac ggc aga gca att aga gaa atc ctt aag aaa cca Thr Gly Lys Ile Asp Gly Arg Ala Ile Arg Glu Ile Leu Lys Lys Pro 530 535 540	1632
gtt gct aag atg Val Ala Lys Met 545	1644

<210> 4
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<212> DNA
<213> Vargula (cypripidina)

<220>
<221> CDS
<222> (1)...(1665)
<223> Vargula (cypripidina) luciferase

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aac tgt caa gat gca tgt cct gta gaa gcg gaa ccg cca tca agt aca Asn Cys Gln Asp Ala Cys Pro Val Glu Ala Glu Pro Pro Ser Ser Thr 20 25 30	96
cca aca gtt cca act tct tgt gaa gct aaa gaa gga gaa tgt ata gat Pro Thr Val Pro Thr Ser Cys Glu Ala Lys Glu Gly Glu Cys Ile Asp 35 40 45	144
acc aga tgc gca aca tgt aaa cga gat ata cta tca gat gga ctg tgt Thr Arg Cys Ala Thr Cys Lys Arg Asp Ile Leu Ser Asp Gly Leu Cys 50 55 60	192
gaa aat aaa cca ggg aag aca tgc tgt aga atg tgc cag tat gtg att Glu Asn Lys Pro Gly Lys Thr Cys Cys Arg Met Cys Gln Tyr Val Ile 65 70 75 80	240
gaa tgc aga gta gaa gca gct ggt tat ttt aga acg ttt tac ggc aaa Glu Cys Arg Val Glu Ala Ala Gly Tyr Phe Arg Thr Phe Tyr Gly Lys 85 90 95	288
aga ttt aat ttt cag gaa cct ggt aaa tat gtg ctg gct agg gga acc Arg Phe Asn Phe Gln Glu Pro Gly Lys Tyr Val Leu Ala Arg Gly Thr 100 105 110	336
aag ggt ggc gat tgg tct gta acc ctc acc atg gag aat cta gat gga Lys Gly Asp Trp Ser Val Thr Leu Thr Met Glu Asn Leu Asp Gly 115 120 125	384
cag aag gga gct gtg ctg act aag aca aca ctg gag gtt gca gga gac Gln Lys Gly Ala Val Leu Thr Lys Thr Leu Glu Val Ala Gly Asp 130 135 140	432
gta ata gac att actcaa gct act gca gat cct atc aca gtt aac gga Val Ile Asp Ile Thr Gln Ala Thr Ala Asp Pro Ile Thr Val Asn Gly 145 150 155 160	480
gga gct gac cca gtt atc gct aac ccg ttc aca att ggt gag gtg acc Gly Ala Asp Pro Val Ile Ala Asn Pro Phe Thr Ile Gly Glu Val Thr 165 170 175	528
att gct gtt gtt gaa ata ccg ggc ttc aat atc aca gtc atc gaa ttc Ile Ala Val Val Glu Ile Pro Gly Phe Asn Ile Thr Val Ile Glu Phe 180 185 190	576
ttt aaa cta atc gtg att gat att ctg gga gga aga tct gtc aga att Phe Lys Leu Ile Val Ile Asp Ile Leu Gly Gly Arg Ser Val Arg Ile 195 200 205	624
gct cca gac aca gca aac aaa gga ctg ata tct ggt atc tgt ggt aat Ala Pro Asp Thr Ala Asn Lys Gly Leu Ile Ser Gly Ile Cys Gly Asn 210 215 220	672
ctg gag atg aat gac gct gat gac ttt act aca gat gca gat cag ctg Leu Glu Met Asn Asp Ala Asp Asp Phe Thr Thr Asp Ala Asp Gln Leu 225 230 235 240	720
gcg atc caa ccc aac ata aac aaa gag ttc gac ggc tgc cca ttc tat Ala Ile Gln Pro Asn Ile Asn Lys Glu Phe Asp Gly Cys Pro Phe Tyr 245 250 255	768
ggc aat cct tct gat atc gaa tac tgc aaa ggt ctg atg gag cca tac	816

Gly Asn Pro Ser Asp Ile Glu Tyr Cys Lys Gly Leu Met Glu Pro Tyr			
260	265	270	
aga gct gta tgt cgt aac aat atc aac ttc tac tat tac act cta tcc			864
Arg Ala Val Cys Arg Asn Asn Ile Asn Phe Tyr Tyr Thr Leu Ser			
275	280	285	
tgt gcc ttc gct tac tgt atg gga gga gaa aga gct aaa cac gtc			912
Cys Ala Phe Ala Tyr Cys Met Gly Gly Glu Arg Ala Lys His Val			
290	295	300	
ctt ttc gac tat gtt gag aca tgc gct gcg ccg gaa acg aga gga acg			960
Leu Phe Asp Tyr Val Glu Thr Cys Ala Ala Pro Glu Thr Arg Gly Thr			
305	310	315	320
tgt gtt tta tca gga cat act ttc tat gac aca ttc gac aaa gca aga			1008
Cys Val Leu Ser Gly His Thr Phe Tyr Asp Thr Phe Asp Lys Ala Arg			
325	330	335	
tat caa ttc cag ggc cca tgc aag gag att ctg atg gcc gca gac tgt			1056
Tyr Gln Phe Gln Gly Pro Cys Lys Glu Ile Leu Met Ala Ala Asp Cys			
340	345	350	
tac tgg aac aca tgg gat gta aag gtt tca cat aga gac gtc gaa tca			1104
Tyr Trp Asn Thr Trp Asp Val Lys Val Ser His Arg Asp Val Glu Ser			
355	360	365	
tac act gag gta gag aaa gta aca atc agg aaa cag tca act gta gta			1152
Tyr Thr Glu Val Glu Lys Val Thr Ile Arg Lys Gln Ser Thr Val Val			
370	375	380	
gat ctc att gtg gat ggc aag cag gtc aag gtt gga gga gtg gat gta			1200
Asp Leu Ile Val Asp Gly Lys Gln Val Lys Val Gly Gly Val Asp Val			
385	390	395	400
tct atc ccg tac agc tct gag aac act tcc ata tac tgg cag gat gga			1248
Ser Ile Pro Tyr Ser Ser Glu Asn Thr Ser Ile Tyr Trp Gln Asp Gly			
405	410	415	
gac atc ctg acg acg gcc atc cta cct gaa gct ctt gtc gtt aag ttc			1296
Asp Ile Leu Thr Ala Ile Leu Pro Glu Ala Leu Val Val Lys Phe			
420	425	430	
aac ttt aag cag ctc ctt gta gtt cat atc aga gat cca ttc gat gca			1344
Asn Phe Lys Gln Leu Leu Val Val His Ile Arg Asp Pro Phe Asp Ala			
435	440	445	
aag aca tgc ggc ata tgt ggt aac tat aat caa gat tca act gat gat			1392
Lys Thr Cys Gly Ile Cys Gly Asn Tyr Asn Gln Asp Ser Thr Asp Asp			
450	455	460	
tcc ttt gac gca gaa gga gca tgc gct cta acc ccc aac ccc cca gga			1440
Phe Phe Asp Ala Glu Gly Ala Cys Ala Leu Thr Pro Asn Pro Pro Gly			
465	470	475	480
tgt aca gag gaa cag aaa cca gaa gct gag cga ctt tgc aat aat ctc			1488
Cys Thr Glu Gln Lys Pro Glu Ala Glu Arg Leu Cys Asn Asn Leu			
485	490	495	
ttt gat tct tct atc gac gag aaa tgt aat gtc tgc tac aag cct gac			1536
Phe Asp Ser Ser Ile Asp Glu Lys Cys Asn Val Cys Tyr Lys Pro Asp			
500	505	510	
cgg att gcc cga tgt atg tac gag tat tgc ctg agg gga caa caa gga			1584
Arg Ile Ala Arg Cys Met Tyr Glu Tyr Cys Leu Arg Gly Gln Gln Gly			

515	520	525	
ttt tgt gac cat gct tgg gag ttc aag aaa gaa tgc tac ata aaa cat Phe Cys Asp His Ala Trp Glu Phe Lys Lys Glu Cys Tyr Ile Lys His 530	535	540	1632
gga gac act cta gaa gta cca cct gaa tgt caa taaaacgtaca aagatacaga Gly Asp Thr Leu Glu Val Pro Pro Glu Cys Gln 545	550	555	1685
agctaaggct actacagcg aagataaaaa agaaaactgta gttccttcaa aaaccgtgta tttatgtac tcattgtta attagagcaa aataaaattgt tattatcata acttaaacta aaaaaaaaaaa aaaaa			1745 1805 1820
<210> 5			
<211> 958			
<212> DNA			
<213> Aequorea victoria			
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<221> CDS			
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<223> Apoequorin-encoding gene			
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gggggggggg gggggggggg gggggggggg gggaatgcaa ttcatctttg catcaaagaa ttacatcaaa tctctagttg atcaactaaa ttgtctcgac aacaacaagg aaac atg 5	10	15	60 Met 1
aca agc aaa caa tac tca gtc aag ctt aca tca gac ttc gac aac cca Thr Ser Lys Gln Tyr Ser Val Lys Leu Thr Ser Asp Phe Asp Asn Pro 5	10	15	117
aga tgg att gga cga cac aag cat atg ttc aat ttc ctt gat gtc aac Arg Trp Ile Gly Arg His Lys Met Phe Asn Phe Leu Asp Val Asn 20	25	30	165 213
cac aat gga aaa atc tct ctt gac gag atg gtc tac aag gca tct gat His Asn Gly Lys Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser Asp 35	40	45	261
att gtc atc aat aac ctt gga gca aca cct gag caa gcc aaa cga cac Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg His 50	55	60	309
aaa gat gct gta gaa gcc ttc ttc gga gga gct gga atg aaa tat ggt Lys Asp Ala Val Glu Ala Phe Phe Gly Ala Gly Met Lys Tyr Gly 70	75	80	357
gtg gaa act gat tgg cct gca tat att gaa gga tgg aaa aaa ttg gct Val Glu Thr Asp Trp Pro Ala Tyr Ile Glu Gly Trp Lys Lys Leu Ala 85	90	95	405
act gat gaa ttg gag aaa tac gcc aaa aac gaa cca acg ctc atc cgt Thr Asp Glu Leu Glu Lys Tyr Ala Lys Asn Glu Pro Thr Leu Ile Arg 100	105	110	453
ata tgg ggt gat gct ttg ttt gat atc gtt gac aaa gat caa aat gga Ile Trp Gly Asp Ala Leu Phe Asp Ile Val Asp Lys Asp Gln Asn Gly 115	120	125	501
gcc att aca ctg gat gaa tgg aaa gca tac acc aaa gct gct ggt atc Ala Ile Thr Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ala Ala Gly Ile 130	135	140	549
			145

gga gct att tca ctg gat gaa tgg aaa gca tac acc aaa tct gat ggc Gly Ala Ile Ser Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ser Asp Gly 130 135 140	432
atc atc caa tcg tca gaa gat tgc gag gaa aca ttc aga gtg tgc gat Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp 145 150 155 160	480
att gat gaa agt gga cag ctc gat gtt gat gag atg aca aga caa cat Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His 165 170 175	528
tta gga ttt tgg tac acc atg gat cct gct tgc gaa aag ctc tac ggt Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly 180 185 190	576
gga gct gtc ccc taa Gly Ala Val Pro 195	591
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cca aga tgg att gga cga cac aag cat atg ttc aat ttc ctt gat gtc Pro Arg Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val 20 25 30	96
aac cac aat gga aaa atc tct ctt gac gag atg gtc tac aag gca tct Asn His Asn Gly Lys Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser 35 40 45	144
gat att gtc atc aat aac ctt gga gca aca cct gag caa gcc aaa cga Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg 50 55 60	192
cac aaa gat gct gta gaa gcc ttc ttc gga gga gct gga atg aaa tat His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Gly Met Lys Tyr 65 70 75 80	240
ggt gtg gaa act gat tgg cct gca tat att gaa gga tgg aaa aaa ttg Gly Val Glu Thr Asp Trp Pro Ala Tyr Ile Glu Gly Trp Lys Lys Leu 85 90 95	288
gct act gat gaa ttg gag aaa tac gcc aaa aac gaa cca acg ctc atc Ala Thr Asp Glu Leu Glu Lys Tyr Ala Lys Asn Glu Pro Thr Leu Ile 100 105 110	336
cgt ata tgg ggt gat gct ttg ttc gat atc gtt gac aaa gat caa aat Arg Ile Trp Gly Asp Ala Leu Phe Asp Ile Val Asp Lys Asp Gln Asn 115 120 125	384

gga gcc att aca ctg gat gaa tgg aaa gca tac acc aaa gct gct ggt Gly Ala Ile Thr Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ala Ala Gly 130 135 140	432
atc atc caa tca tca gaa qat tgc gag gaa aca ttc aga gtg tgc gat Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp 145 150 155 160	480
att gat gaa agt gga caa ctc gat gtt gat gag atg aca aga caa cat Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His 165 170 175	528
tta gga ttt tgg tac acc atg gat cct gct tgc gaa aag ctc tac ggt Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly 180 185 190	576
gga gct gtc ccc taa Gly Ala Val Pro 195	591
<210> 8	
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<221> CDS	
<222> (1)...(588)	
<223> Recombinant Aequorin AEQ3	
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cca aga tgg att gga cga cac aag cat atg ttc aat ttc ctt gat gtc Pro Arg Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val 20 25 30	96
aac cac aat gga aaa atc tct ctt gac gag atg gtc tac aag gca tct Asn His Asn Gly Lys Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser 35 40 45	144
gat att gtc atc aat aac ctt gga gca aca cct gag caa gcc aaa cga Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg 50 55 60	192
cac aaa gat gct gta gga gac ttc ttc gga gga gct gga atg aaa tat His Lys Asp Ala Val Gly Asp Phe Phe Gly Gly Ala Gly Met Lys Tyr 65 70 75 80	240
ggt gtg gaa act gat tgg cct gca tac att gaa gga tgg aaa aaa ttg Gly Val Glu Thr Asp Trp Pro Ala Tyr Ile Glu Gly Trp Lys Lys Leu 85 90 95	288
gct act gat gaa ttg gag aaa tac gcc aaa aac gaa cca acg ctc atc Ala Thr Asp Glu Leu Glu Lys Tyr Ala Lys Asn Glu Pro Thr Leu Ile 100 105 110	336
cgt ata tgg ggt gat gct ttg ttc gat atc gtt gac aaa gat caa aat Arg Ile Trp Gly Asp Ala Leu Phe Asp Ile Val Asp Lys Asp Gln Asn 115 120 125	384
gga gcc att aca ctg gat gaa tgg aaa gca tac acc aaa gct gct ggt	432

Gly Ala Ile Thr Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ala Ala Gly
 130 135 140

atc atc caa tca tca gaa gat tgc gag gaa aca ttc aga gtg tgc gat 480
 Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp
 145 150 155 160

att gat gaa aat gga caa ctc gat gtt gat gag atg aca aga caa cat 528
 Ile Asp Glu Asn Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His
 165 170 175

tta gga ttt tgg tac acc atg gat cct gct tgc gaa aag ctc tac ggt 576
 Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly
 180 185 190

gga gct gtc ccc taa 591
 Gly Ala Val Pro
 195

<210> 9
 <211> 567
 <212> DNA
 <213> Aequoria victoria

<220>
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 <222> (1) ... (567)
 <223> Aequorin photoprotein

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 Val Lys Leu Thr Pro Asp Phe Asp Asn Pro Lys Trp Ile Gly Arg His
 1 5 10 15

aag cac atg ttt aat ttt ctt gat gtc aac cac aat gga agg atc tct 96
 Lys His Met Phe Asn Phe Leu Asp Val Asn His Asn Gly Arg Ile Ser
 20 25 30

ctt gac gag atg gtc tac aag gcg tcc gat att gtt ata aac aat ctt 144
 Leu Asp Glu Met Val Tyr Lys Ala Ser Asp Ile Val Ile Asn Asn Leu
 35 40 45

gga gca aca cct gaa caa gcc aaa cgt cac aaa gat gct gta gaa gcc 192
 Gly Ala Thr Pro Glu Gln Ala Lys Arg His Lys Asp Ala Val Glu Ala
 50 55 60

ttc ttc gga gga gct gca atg aaa tat ggt gta gaa act gaa tgg cct 240
 Phe Phe Gly Gly Ala Ala Met Lys Tyr Gly Val Glu Thr Glu Trp Pro
 65 70 75 80

gaa tac atc gaa gga tgg aaa aga ctg gct tcc gag gaa ttg aaa agg 288
 Glu Tyr Ile Glu Gly Trp Lys Arg Leu Ala Ser Glu Glu Leu Lys Arg
 85 90 95

tat tca aaa aac caa atc aca ctt att cgt tta tgg ggt gat gca ttg 336
 Tyr Ser Lys Asn Gln Ile Thr Leu Ile Arg Leu Trp Gly Asp Ala Leu
 100 105 110

ttc gat atc att gac aaa gac caa aat gga gct att tca ctg gat gaa 384
 Phe Asp Ile Ile Asp Lys Asp Gln Asn Gly Ala Ile Ser Leu Asp Glu
 115 120 125

tgg aaa gca tac acc aaa tct gct ggc atc atc caa tcg tca gaa gat 432
 Trp Lys Ala Tyr Thr Lys Ser Ala Gly Ile Ile Gln Ser Ser Glu Asp
 130 135 140

tgc gag gaa aca ttc aga gtg tgc gat att gat gaa agt gga cag ctc Cys Glu Glu Thr Phe Arg Val Cys Asp Ile Asp Glu Ser Gly Gln Leu 145 150 155 160	480
gat gtt gat gag atg aca aga caa cat tta gga ttt tgg tac acc atg Asp Val Asp Glu Met Thr Arg Gln His Leu Gly Phe Trp Tyr Thr Met 165 170 175	528
gat cct gct tgc gaa aag ctc tac ggt gga gct gtc ccc Asp Pro Ala Cys Glu Lys Leu Tyr Gly Gly Ala Val Pro 180 185	567
<210> 10	
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<223> Aequorin mutant w/increased bioluminescence activity	
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cca aaa tgg att gga cga cac aag cac atg ttt aat ttt ctt gat gtc Pro Lys Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val 20 25 30	96
aac cac aat gga agg atc tct ctt gac gag atg gtc tac aag gcg tcc Asn His Asn Gly Arg Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser 35 40 45	144
gat att gtt ata aac aat ctt gga gca aca cct gaa caa gcc aaa cgt Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg 50 55 60	192
cac aaa gat gct gta gaa gcc ttc ttc gga gga gct gca atg aaa tat His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Ala Met Lys Tyr 65 70 75 80	240
ggg gta gaa act gaa tgg cct gaa tac atc gaa gga tgg aaa aga ctg Gly Val Glu Thr Glu Trp Pro Glu Tyr Ile Glu Gly Trp Lys Arg Leu 85 90 95	288
gct tcc gag gaa ttg aaa agg tat tca aaa aac caa atc aca ctt att Ala Ser Glu Glu Leu Lys Arg Tyr Ser Lys Asn Gln Ile Thr Leu Ile 100 105 110	336
cgt tta tgg ggt gat gca ttg ttc gat atc att tcc aaa gac caa aat Arg Leu Trp Gly Asp Ala Leu Phe Asp Ile Ile Ser Lys Asp Gln Asn 115 120 125	384
gga gct att tca ctg gat gaa tgg aaa gca tac acc aaa tct gct ggc Gly Ala Ile Ser Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ser Ala Gly 130 135 140	432
atc atc caa tcg tca gaa gat tgc gag gaa aca ttc aga gtg tgc gat Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp 145 150 155 160	480

att gat gaa agt gga cag ctc gat gtt gat gag atg aca aga caa cat Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His 165 170 175	528
tta gga ttt tgg tac acc atg gat cct gct tgc gaa aag ctc tac ggt Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly 180 185 190	576
gga gct gtc ccc Gly Ala Val Pro 195	588
<210> 11	
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<213> Aequorea victoria	
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<221> CDS	
<222> (1) ... (588)	
<223> Recombinant site-directed Aequorin mutant	
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cca aaa tgg att gga cga cac aag cac atg ttt aat ttt ctt gat gtc Pro Lys Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val 20 25 30	96
aac cac aat gga agg atc tct ctt gac gag atg gtc tac aag gcg tcc Asn His Asn Gly Arg Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser 35 40 45	144
gat att gtt ata aac aat ctt gga gca aca cct gaa caa gcc aaa cgt Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg 50 55 60	192
cac aaa gat gct gta gaa gcc ttc ttc gga gga gct gca atg aaa tat His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Ala Met Lys Tyr 65 70 75 80	240
ggt gta gaa act gaa tgg cct gaa tac atc gaa gga tgg aaa aga ctg Gly Val Glu Thr Glu Trp Pro Glu Tyr Ile Glu Gly Trp Lys Arg Leu 85 90 95	288
gct tcc gag gaa ttg aaa agg tat tca aaa aac caa atc aca ctt att Ala Ser Glu Glu Leu Lys Arg Tyr Ser Lys Asn Gln Ile Thr Leu Ile 100 105 110	336
cgt tta tgg ggt gat gca ttg ttc gat atc att tcc aaa gac caa aat Arg Leu Trp Gly Asp Ala Leu Phe Asp Ile Ile Ser Lys Asp Gln Asn 115 120 125	384
gga gct att tca ctg gat tca tgg aaa gca tac acc aaa tct gct ggc Gly Ala Ile Ser Leu Asp Ser Trp Lys Ala Tyr Thr Lys Ser Ala Gly 130 135 140	432
atc atc caa tcg tca gaa gat tgc gag gaa aca ttc aga gtg tgc gat Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp 145 150 155 160	480

att gat gaa agt gga cag ctc gat gtt gat gag atg aca aga caa cat Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His 165 170 175	528
tta gga ttt tgg tac acc atg gat cct gct tgc gaa aag ctc tac ggt Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly 180 185 190	576
gga gct gtc ccc Gly Ala Val Pro 195	588
 <210> 12	
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<223> Aequorin mutant with increased bioluminescence activity	
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cca aaa tgg att gga cga cac aag cac atg ttt aat ttt ctt gat gtc Pro Lys Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val 20 25 30	96
aac cac aat gga agg atc tct ctt gac gag atg gtc tac aag gcg tcc Asn His Asn Gly Arg Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser 35 40 45	144
gat att gtt ata aac aat ctt gga gca aca cct gaa caa gcc aaa cgt Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg 50 55 60	192
cac aaa gat gct gta gaa gcc ttc gga gga gct gca atg aaa tat His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Ala Met Lys Tyr 65 70 75 80	240
ggg gta gaa act gaa tgg cct gaa tac atc gaa gga tgg aaa aga ctg Gly Val Glu Thr Glu Trp Pro Glu Tyr Ile Glu Gly Trp Lys Arg Leu 85 90 95	288
gct tcc gag gaa ttg aaa agg tat tca aaa aac caa atc aca ctt att Ala Ser Glu Glu Leu Lys Arg Tyr Ser Lys Asn Gln Ile Thr Leu Ile 100 105 110	336
cgt tta tgg ggt gat gca ttg ttc gat atc att tcc aaa gac caa aat Arg Leu Trp Gly Asp Ala Leu Phe Asp Ile Ile Ser Lys Asp Gln Asn 115 120 125	384
gca gct att tca ctg gat gaa tgg aaa gca tac acc aaa tct gct ggc Ala Ala Ile Ser Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ser Ala Gly 130 135 140	432
atc atc caa tcg tca gaa gat tgc gag gaa aca ttc aga gtg tgc gat Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp 145 150 155 160	480

att gat gaa agt gga cag ctc gat gtt gat gag atg aca aga caa cat Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His 165 170 175	528
tta gga ttt tgg tac acc atg gat cct gct tgc gaa aag ctc tac ggt Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly 180 185 190	576
gga gct gtc ccc Gly Ala Val Pro 195	588
<210> 13	
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<223> Recombinant apoaequorin (AQUALITEP)	
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aag cac atg ttt aat ttt ctt gat gtc aac cac aat gga agg atc tct Lys His Met Phe Asn Phe Leu Asp Val Asn His Asn Gly Arg Ile Ser 20 25 30	96
ctt gac gag atg gtc tac aag gcg tcc gat att gtt ata aac aat ctt Leu Asp Glu Met Val Tyr Lys Ala Ser Asp Ile Val Ile Asn Asn Leu 35 40 45	144
gga gca aca cct gaa caa gcc aaa cgt cac aaa gat gct gta gaa gcc Gly Ala Thr Pro Glu Gln Ala Lys Arg His Lys Asp Ala Val Glu Ala 50 55 60	192
ttc ttc gga gga gct gga atg aaa tat ggt gta gaa act gaa tgg cct Phe Phe Gly Gly Ala Gly Met Lys Tyr Gly Val Glu Thr Glu Trp Pro 65 70 75 80	240
gaa tac atc gaa gga tgg aaa aaa ctg gct tcc gag gaa ttg aaa agg Glu Tyr Ile Glu Gly Trp Lys Lys Leu Ala Ser Glu Glu Leu Lys Arg 85 90 95	288
tat tca aaa aac caa atc aca ctt att cgt tta tgg ggt gat gca ttg Tyr Ser Lys Asn Gln Ile Thr Leu Ile Arg Leu Trp Gly Asp Ala Leu 100 105 110	336
ttc gat atc att gac aaa gac caa aat gga gct att ctg tca gat gaa Phe Asp Ile Ile Asp Lys Asp Gln Asn Gly Ala Ile Leu Ser Asp Glu 115 120 125	384
tgg aaa gca tac acc aaa tct gat ggc atc atc caa tcg tca gaa gat Trp Lys Ala Tyr Thr Lys Ser Asp Gly Ile Ile Gln Ser Ser Glu Asp 130 135 140	432
tgc gag gaa aca ttc aga gtg tgc gat att gat gaa agt gga cag ctc Cys Glu Glu Thr Phe Arg Val Cys Asp Ile Asp Glu Ser Gly Gln Leu 145 150 155 160	480
gat gtt gat gag atg aca aga caa cat tta gga ttt tgg tac acc atg	528

Asp Val Asp Glu Met Thr Arg Gln His Leu Gly Phe Trp Tyr Thr Met
 165 170 175

gat cct gct tgc gaa aag ctc tac ggt gga gct gtc ccc
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 180 185

<210> 14
 <211> 236
 <212> PRT
 <213> Vibrio fisheri

<400> 14

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 Thr Phe Arg Ile Leu Leu His Pro Glu Gln Pro Val Ala Phe Lys Ala
 20 25 30
 Gly Gln Tyr Leu Thr Val Val Met Gly Glu Lys Asp Lys Arg Pro Phe
 35 40 45
 Ser Ile Ala Ser Ser Pro Cys Arg His Glu Gly Glu Ile Glu Leu His
 50 55 60
 Ile Gly Ala Ala Glu His Asn Ala Tyr Ala Gly Glu Val Val Glu Ser
 65 70 75 80
 Met Lys Ser Ala Leu Glu Thr Gly Gly Asp Ile Leu Ile Asp Ala Pro
 85 90 95
 His Gly Glu Ala Trp Ile Arg Glu Asp Ser Asp Arg Ser Met Leu Leu
 100 105 110
 Ile Ala Gly Gly Thr Gly Phe Ser Tyr Val Arg Ser Ile Leu Asp His
 115 120 125
 Cys Ile Ser Gln Gln Ile Gln Lys Pro Ile Tyr Leu Tyr Trp Gly Gly
 130 135 140
 Arg Asp Glu Cys Gln Leu Tyr Ala Lys Ala Glu Leu Glu Ser Ile Ala
 145 150 155 160
 Gln Ala His Ser His Ile Thr Phe Val Pro Val Val Glu Lys Ser Glu
 165 170 175
 Gly Trp Thr Gly Lys Thr Gly Asn Val Leu Glu Ala Val Lys Ala Asp
 180 185 190
 Phe Asn Ser Leu Ala Asp Met Asp Ile Tyr Ile Ala Gly Arg Phe Glu
 195 200 205
 Met Ala Gly Ala Ala Arg Glu Gln Phe Thr Thr Glu Lys Gln Ala Lys
 210 215 220
 Lys Glu Gln Leu Phe Gly Asp Ala Phe Ala Phe Ile
 225 230 235

<210> 15
 <211> 1079
 <212> DNA
 <213> Renilla mulleri

<220>
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 <222> (259)...(975)
 <223> Renilla mulleri GFP

<400> 15

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 acataatatc taagagacgc ctcatattaag agtagaaaa atataatata tgatagagta
 tacaactctc gccttagaca gagagtgtgc aacagagtaa ctcttgtaa tgcaatcgaa
 agcgtcaaga gagataag atg agt aaa caa ata ttg aag aac act tgt tta
 Met Ser Lys Gln Ile Leu Lys Asn Thr Cys Leu
 1 5 10

caa gaa gta atg tcg tat aaa gta aat ctg gaa gga att gta aac aac Gln Glu Val Met Ser Tyr Lys Val Asn Leu Glu Gly Ile Val Asn Asn 15 20 25	339
cat gtt ttt aca atg gag ggt tgc ggc aaa ggg aat att tta ttc ggc His Val Phe Thr Met Glu Gly Cys Gly Lys Gly Asn Ile Leu Phe Gly 30 35 40	387
aat cca ctg gtt cag att cgt gtc acg aaa ggg gcc cca ctg cct ttt Asn Gln Leu Val Gln Ile Arg Val Thr Lys Gly Ala Pro Leu Pro Phe 45 50 55	435
gca ttt gat att gtg tca cca gct ttt caa tat ggc aac cgt act ttc Ala Phe Asp Ile Val Ser Pro Ala Phe Gln Tyr Gly Asn Arg Thr Phe 60 65 70 75	483
acg aaa tat ccg aat gat ata tca gat tat ttt ata caa tca ttt cca Thr Lys Tyr Pro Asn Asp Ile Ser Asp Tyr Phe Ile Gln Ser Phe Pro 80 85 90	531
gca gga ttt atg tat gaa cga aca tta cgt tac gaa gat ggc gga ctt Ala Gly Phe Met Tyr Glu Arg Thr Leu Arg Tyr Glu Asp Gly Gly Leu 95 100 105	579
gtt gaa att cgt tca gat ata aat tta ata gaa gac aag ttc gtc tac Val Glu Ile Arg Ser Asp Ile Asn Leu Ile Glu Asp Lys Phe Val Tyr 110 115 120	627
aga gtg gaa tac aaa ggt agt aac ttc cca gat gat ggt ccc gtc atg Arg Val Glu Tyr Lys Gly Ser Asn Phe Pro Asp Asp Gly Pro Val Met 125 130 135	675
cag aag act atc tta gga ata gag cct tca ttt gaa gcc atg tac atg Gln Lys Thr Ile Leu Gly Ile Glu Pro Ser Phe Glu Ala Met Tyr Met 140 145 150 155	723
aat aat ggc gtc ttg gtc ggc gaa gta att ctt gtc tat aaa cta aac Asn Asn Gly Val Leu Val Gly Glu Val Ile Leu Val Tyr Lys Leu Asn 160 165 170	771
tct ggg aaa tat tat tca tgt cac atg aaa aca tta atg aag tcg aaa Ser Gly Lys Tyr Tyr Ser Cys His Met Lys Thr Leu Met Lys Ser Lys 175 180 185	819
ggt gta gta aag gag ttt cct tcg tat cat ttt att caa cat cgt ttg Gly Val Val Lys Glu Phe Pro Ser Tyr His Phe Ile Gln His Arg Leu 190 195 200	867
gaa aag act tac gta gaa gac ggg ggg ttc gtt gaa cag cat gag act Glu Lys Thr Tyr Val Glu Asp Gly Gly Phe Val Glu Gln His Glu Thr 205 210 215	915
gct att gct caa atg aca tct ata gga aaa cca cta gga tcc tta cac Ala Ile Ala Gln Met Thr Ser Ile Gly Lys Pro Leu Gly Ser Leu His 220 225 230 235	963
gaa tgg gtt taa acacagttac attactttt ccaattcgta tttcatgtca Glu Trp Val *	1015
aataataatt ttttaaacaa ttatcaatgt tttgtgatat gtttgtaaaa aaaaaaaaaa aaaa	1075 1079

<210> 16
<211> 238

<212> PRT

<213> Renilla mulleri

<400> 16
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 1 5 10 15
 Tyr Lys Val Asn Leu Glu Gly Ile Val Asn Asn His Val Phe Thr Met
 20 25 30
 Glu Gly Cys Gly Lys Gly Asn Ile Leu Phe Gly Asn Gln Leu Val Gln
 35 40 45
 Ile Arg Val Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val
 50 55 60
 Ser Pro Ala Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr Pro Asn
 65 70 75 80
 Asp Ile Ser Asp Tyr Phe Ile Gln Ser Phe Pro Ala Gly Phe Met Tyr
 85 90 95
 Glu Arg Thr Leu Arg Tyr Glu Asp Gly Gly Leu Val Glu Ile Arg Ser
 100 105 110
 Asp Ile Asn Leu Ile Glu Asp Lys Phe Val Tyr Arg Val Glu Tyr Lys
 115 120 125
 Gly Ser Asn Phe Pro Asp Asp Gly Pro Val Met Gln Lys Thr Ile Leu
 130 135 140
 Gly Ile Glu Pro Ser Phe Glu Ala Met Tyr Met Asn Asn Gly Val Leu
 145 150 155 160
 Val Gly Glu Val Ile Leu Val Tyr Lys Leu Asn Ser Gly Lys Tyr Tyr
 165 170 175
 Ser Cys His Met Lys Thr Leu Met Lys Ser Lys Gly Val Val Lys Glu
 180 185 190
 Phe Pro Ser Tyr His Phe Ile Gln His Arg Leu Glu Lys Thr Tyr Val
 195 200 205
 Glu Asp Gly Gly Phe Val Glu Gln His Glu Thr Ala Ile Ala Gln Met
 210 215 220
 Thr Ser Ile Gly Lys Pro Leu Gly Ser Leu His Glu Trp Val
 225 230 235

<210> 17

<211> 1217

<212> DNA

<213> Renilla mulleri

<220>

<221> CDS

<222> (31)...(963)

<223> Renilla mulleri luciferase

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 gaa tta aga aaa cgc atg att act ggt cca caa tgg tgg gca aga tgt 102
 Glu Leu Arg Lys Arg Met Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys
 10 15 20
 aaa caa atg aat gtt ctt gat tca ttt att aat tat tat gat tca gaa 150
 Lys Gln Met Asn Val Leu Asp Ser Phe Ile Asn Tyr Tyr Asp Ser Glu
 25 30 35 40
 aaa cat gca gaa aat gca gtt ata ttt tta cat ggt aat gca gca tct 198
 Lys His Ala Glu Asn Ala Val Ile Phe Leu His Gly Asn Ala Ala Ser
 45 50 55
 tct tat tta tgg cgt cat gtt gta cca cat gtt gaa cca gtg gcg cga 246
 Ser Tyr Ile Trp Arg His Val Val Pro His Val Glu Pro Val Ala Arg
 60 65 70

tgt att ata cca gat ctt ata ggt atg ggt aaa tca ggc aag tct ggt Cys Ile Ile Pro Asp Leu Ile Gly Met Gly Lys Ser Gly Lys Ser Gly 75 80 85	294
aat ggt tcc tat aga tta cta gat cat tac aaa tat ctt act gaa tgg Asn Gly Ser Tyr Arg Leu Leu Asp His Tyr Lys Tyr Leu Thr Glu Trp 90 95 100	342
ttc aaa cat ctt aat tta cca aag aag atc att ttt gtc ggt cat gat Phe Lys His Leu Asn Leu Pro Lys Lys Ile Ile Phe Val Gly His Asp 105 110 115 120	390
tgg ggt gct tgt tta gca ttt cat tat tgc tat gaa cat cag gat cgc Trp Gly Ala Cys Leu Ala Phe His Tyr Cys Tyr Glu His Gln Asp Arg 125 130 135	438
atc aaa gca gtt gtt cat gct gaa agt gta gta gat gtg att gaa tcg Ile Lys Ala Val Val His Ala Glu Ser Val Val Asp Val Ile Glu Ser 140 145 150	486
tgg gac gaa tgg cct gat att gaa gaa gat att gct ttg att aaa tct Trp Asp Glu Trp Pro Asp Ile Glu Glu Asp Ile Ala Leu Ile Lys Ser 155 160 165	534
gaa gaa gga gaa aaa atg gtt tta gag aat aac ttc ttc gtg gaa acc Glu Glu Gly Glu Lys Met Val Leu Glu Asn Asn Phe Phe Val Glu Thr 170 175 180	582
atg ttg cca tca aaa atc atg aga aag ttg gaa cca gag gaa ttt gct Met Leu Pro Ser Lys Ile Met Arg Lys Leu Glu Pro Glu Glu Phe Ala 185 190 195 200	630
gct tat ctt gaa cca ttt aaa gag aaa ggt gaa gtt cgt cgt cca aca Ala Tyr Leu Glu Pro Phe Lys Glu Lys Gly Glu Val Arg Arg Pro Thr 205 210 215	678
tta tca tgg cct cgt gaa atc cct ttg gta aaa ggt ggt aaa ccg gat Leu Ser Trp Pro Arg Glu Ile Pro Leu Val Lys Gly Gly Lys Pro Asp 220 225 230	726
gta gta gaa att gtc agg aat tat aat gct tat ctt cgt gca agt cat Val Val Glu Ile Val Arg Asn Tyr Asn Ala Tyr Leu Arg Ala Ser His 235 240 245	774
gat tta cca aaa atg ttt att gaa tct gat cca gga ttc ttt tcc aat Asp Leu Pro Lys Met Phe Ile Glu Ser Asp Pro Gly Phe Phe Ser Asn 250 255 260	822
gct att gtt gaa ggt gct aag aaa ttc cct aat act gaa ttt gtt aaa Ala Ile Val Glu Gly Ala Lys Lys Phe Pro Asn Thr Glu Phe Val Lys 265 270 275 280	870
gtc aaa ggt ctt cat ttt tca caa gaa gat gca cct gat gaa atg gga Val Lys Gly Leu His Phe Ser Gln Glu Asp Ala Pro Asp Glu Met Gly 285 290 295	918
aat tat ata aaa tcg ttt gtt gag cgt gtt ctt aaa aat gaa caa Asn Tyr Ile Lys Ser Phe Val Glu Arg Val Leu Lys Asn Glu Gln 300 305 310	963
taaactacca ggtttccatg ttgccacttt agctgggttt aataaaatttc actatcaatt tgaacaattt cacattaatt ttaactatta aaaaattatg gacacaggga ttatatcaga tgattaattt agttgggaac aatgaatacc gaatattatg aattctcttt agctatttat aataatcaca ttcttatgta ataaaaacttt gtttaataa attaatgatt cagaaaaaaaa	1023 1083 1143 1203

aaaaaaaaaa aaaa

1217

<210> 18

<211> 311

<212> PRT

<213> Renilla mulleri

<400> 18

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			20					25					30		
Phe	Ile	Asn	Tyr	Tyr	Asp	Ser	Glu	Lys	His	Ala	Glu	Asn	Ala	Val	Ile
	35					40						45			
Phe	Leu	His	Gly	Asn	Ala	Ala	Ser	Ser	Tyr	Leu	Trp	Arg	His	Val	Val
	50						55				60				
Pro	His	Val	Glu	Pro	Val	Ala	Arg	Cys	Ile	Ile	Pro	Asp	Leu	Ile	Gly
65					70					75					80
Met	Gly	Lys	Ser	Gly	Lys	Ser	Gly	Asn	Gly	Ser	Tyr	Arg	Leu	Leu	Asp
	85						90						95		
His	Tyr	Lys	Tyr	Leu	Thr	Glu	Trp	Phe	Lys	His	Leu	Asn	Leu	Pro	Lys
	100					105						110			
Lys	Ile	Ile	Phe	Val	Gly	His	Asp	Trp	Gly	Ala	Cys	Leu	Ala	Phe	His
	115					120					125				
Tyr	Cys	Tyr	Glu	His	Gln	Asp	Arg	Ile	Lys	Ala	Val	Val	His	Ala	Glu
	130					135					140				
Ser	Val	Val	Asp	Val	Ile	Glu	Ser	Trp	Asp	Glu	Trp	Pro	Asp	Ile	Glu
145					150					155					160
Glu	Asp	Ile	Ala	Leu	Ile	Lys	Ser	Glu	Glu	Gly	Glu	Lys	Met	Val	Leu
	165					170					175				
Glu	Asn	Asn	Phe	Val	Glu	Thr	Met	Leu	Pro	Ser	Lys	Ile	Met	Arg	
	180					185					190				
Lys	Leu	Glu	Pro	Glu	Glu	Phe	Ala	Ala	Tyr	Leu	Glu	Pro	Phe	Lys	Glu
	195					200					205				
Lys	Gly	Glu	Val	Arg	Arg	Pro	Thr	Leu	Ser	Trp	Pro	Arg	Glu	Ile	Pro
210						215					220				
Leu	Val	Lys	Gly	Gly	Lys	Pro	Asp	Val	Val	Glu	Ile	Val	Arg	Asn	Tyr
225					230					235					240
Asn	Ala	Tyr	Leu	Arg	Ala	Ser	His	Asp	Leu	Pro	Lys	Met	Phe	Ile	Glu
	245						250					255			
Ser	Asp	Pro	Gly	Phe	Phe	Ser	Asn	Ala	Ile	Val	Glu	Gly	Ala	Lys	Lys
	260					265					270				
Phe	Pro	Asn	Thr	Glu	Phe	Val	Lys	Val	Lys	Gly	Leu	His	Phe	Ser	Gln
	275					280					285				
Glu	Asp	Ala	Pro	Asp	Glu	Met	Gly	Asn	Tyr	Ile	Lys	Ser	Phe	Val	Glu
	290					295					300				
Arg	Val	Leu	Lys	Asn	Glu	Gln									
	305					310									

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<211> 765

<212> DNA

<213> Gaussia

<220>

<221> CDS

<222> (37) ... (594)

<400> 19

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				Met	Gly	Val	Lys	Val	Leu
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54

ttt	gcc	ctt	att	tgt	att	gct	gtg	gcc	gag	gcc	aaa	cca	act	gaa	aac
Phe	Ala	Leu	Ile	Cys	Ile	Ala	Val	Ala	Glu	Ala	Lys	Pro	Thr	Glu	Asn

102

10	15	20	
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gat ctc gat gct gac cgt ggt aaa ttg ccc gga aaa aaa tta cca ctt Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro Gly Lys Lys Leu Pro Leu 40 45 50			198
gag gta ctc aaa gaa atg gaa gcc aat gct agg aaa gct ggc tgc act Glu Val Leu Lys Glu Met Glu Ala Asn Ala Arg Lys Ala Gly Cys Thr 55 60 65 70			246
agg gga tgt ctg ata tgc ctg tca cac atc aag tgt aca ccc aaa atg Arg Gly Cys Leu Ile Cys Leu Ser His Ile Lys Cys Thr Pro Lys Met 75 80 85			294
aag aag ttt atc cca gga aga tgc cac acc tat gaa gga gac aaa gaa Lys Lys Phe Ile Pro Gly Arg Cys His Thr Tyr Glu Gly Asp Lys Glu 90 95 100			342
agt gca cag gga gga ata gga gag gct att gtt gac att cct gaa att Ser Ala Gln Gly Ile Gly Glu Ala Ile Val Asp Ile Pro Glu Ile 105 110 115			390
cct ggg ttt aag gat ttg gaa ccc atg gaa caa ttc att gca caa gtt Pro Gly Phe Lys Asp Leu Glu Pro Met Glu Gln Phe Ile Ala Gln Val 120 125 130			438
gac cta tgt gta gac tgc aca act gga tgc ctc aaa ggt ctt gcc aat Asp Leu Cys Val Asp Cys Thr Thr Gly Cys Leu Lys Gly Leu Ala Asn 135 140 145 150			486
gtg caa tgt tct gat tta ctc aag aaa tgg ctg cca caa aga tgt gca Val Gln Cys Ser Asp Leu Leu Lys Lys Trp Leu Pro Gln Arg Cys Ala 155 160 165			534
act ttt gct agc aaa att caa ggc caa gtg gac aaa ata aag ggt gcc Thr Phe Ala Ser Lys Ile Gln Gly Gln Val Asp Lys Ile Lys Gly Ala 170 175 180			582
ggt ggt gat taa tcctaataaga atactgcata actggatgtat gatatactag Gly Gly Asp *185			634
cttattgctc ataaaatggc catttttgt aacaaatcga gtctatgtaa ttcaaaatac ctaattaatt gttaatacat atgttaattcc tataaatata atttatgcaa tccaaaaaaaa aaaaaaaaaa a			694 754 765
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65	70	75	80
Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro Gly Arg Cys His Thr			
85	90	95	
Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile			
100	105	110	
Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu			
115	120	125	
Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys			
130	135	140	
Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp			
145	150	155	160
Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val			
165	170	175	
Asp Lys Ile Lys Gly Ala Gly Asp			
180	185		

<210> 21
<211> 1146
<212> DNA
<213> Gaussia

<220>
<221> CDS
<222> (1)...(1146)
<223> Nucleotide sequence encoding a CBD-Gaussia luciferase fusion protein

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1	5	10	15
att aca cca ata atc aaa att act aac aca tct gac agt gat tta aat		96	
Ile Thr Pro Ile Ile Lys Ile Thr Asn Thr Ser Asp Ser Asp Leu Asn			
20	25	30	
tta aat gac gta aaa gtt aga tat tat tac aca agt gat ggt aca caa		144	
Leu Asn Asp Val Lys Val Arg Tyr Tyr Tyr Thr Ser Asp Gly Thr Gln			
35	40	45	
gga caa act ttc tgg tgt gac cat gct ggt gca tta tta gga aat agc		192	
Gly Gln Thr Phe Trp Cys Asp His Ala Gly Ala Leu Leu Gly Asn Ser			
50	55	60	
tat gtt gat aac act agc aaa gtg aca gca aac ttc gtt aaa gaa aca		240	
Tyr Val Asp Asn Thr Ser Lys Val Thr Ala Asn Phe Val Lys Glu Thr			
65	70	75	80
gca agc cca aca tca acc tat gat aca tat gtt gaa ttt gga ttt gca		288	
Ala Ser Pro Thr Ser Thr Tyr Asp Thr Tyr Val Glu Phe Gly Phe Ala			
85	90	95	
agc gga gca gct act ctt aaa aaa gga caa ttt ata act att caa gga		336	
Ser Gly Ala Ala Thr Leu Lys Lys Gly Gln Phe Ile Thr Ile Gln Gly			
100	105	110	
aga ata aca aaa tca gac tgg tca aac tac act caa aca aat gac tat		384	
Arg Ile Thr Lys Ser Asp Trp Ser Asn Tyr Thr Gln Thr Asn Asp Tyr			
115	120	125	
tca ttt gat gca agt agt tca aca cca gtt gta aat cca aaa gtt aca		432	
Ser Phe Asp Ala Ser Ser Thr Pro Val Val Asn Pro Lys Val Thr			
130	135	140	
gga tat ata ggt gga gct aaa gtt ctt ggt aca gca cca ggt tcc gcg		480	

Gly Tyr Ile Gly Gly Ala Lys Val Leu Gly Thr Ala Pro Gly Ser Ala																																																																																																																																																																													
145	150	155	160			ggt ctg gtg cca cgc ggt agt act gca att ggt atg aaa gaa acc gct			528	Gly Leu Val Pro Arg Gly Ser Thr Ala Ile Gly Met Lys Glu Thr Ala				165	170	175		gct gct aaa ttc gaa cgc cag cac atg gac agc cca gat ctg ggt acc			576	Ala Ala Lys Phe Glu Arg Gln His Met Asp Ser Pro Asp Leu Gly Thr				180	185	190		gat gac gac gac aag atg gga gtg aaa gtt ctt ttt gcc ctt att tgt			624	Asp Asp Asp Lys Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys				195	200	205		att gct gtg gcc gag gcc aaa cca act gaa aac aat gaa gat ttc aac			672	Ile Ala Val Ala Glu Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn				210	215	220		att gta gct gta gct agc aac ttt gct aca acg gat ctc gat gct gac			720	Ile Val Ala Val Ala Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp				225	230	235	240	cgt ggt aaa ttg ccc gga aaa aaa tta cca ctt gag gta ctc aaa gaa			768	Arg Gly Lys Leu Pro Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu				245	250	255		atg gaa gcc aat gct agg aaa gct ggc tgc act agg gga tgt ctg ata			816	Met Glu Ala Asn Ala Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile				260	265	270		tgc ctg tca cac atc aag tgt aca ccc aaa atg aag aag ttt atc cca			864	Cys Leu Ser His Ile Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro				275	280	285		gga aga tgc cac acc tat gaa gga gac aaa gaa agt gca cag gga gga			912	Gly Arg Cys His Thr Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly				290	295	300		ata gga gag gct att gtt gac att cct gaa att cct ggg ttt aag gat			960	Ile Gly Glu Ala Ile Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp				305	310	315	320	ttg gaa ccc atg gaa caa ttc att gca caa gtt gac cta tgt gta gac			1008	Leu Glu Pro Met Glu Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp				325	330	335		tgc aca act gga tgc ctc aaa ggt ctt gcc aat gtg caa tgt tct gat			1056	Cys Thr Thr Gly Cys Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp				340	345	350		tta ctc aag aaa tgg ctg cca caa aga tgt gca act ttt gct agc aaa			1104	Leu Leu Lys Lys Trp Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys				355	360	365		att caa ggc caa gtg gac aaa ata aag ggt gcc ggt ggt gat			1146	Ile Gln Gly Gln Val Asp Lys Ile Lys Gly Ala Gly Gly Asp				370	375	380	
160																																																																																																																																																																													
ggt ctg gtg cca cgc ggt agt act gca att ggt atg aaa gaa acc gct			528																																																																																																																																																																										
Gly Leu Val Pro Arg Gly Ser Thr Ala Ile Gly Met Lys Glu Thr Ala																																																																																																																																																																													
165	170	175																																																																																																																																																																											
gct gct aaa ttc gaa cgc cag cac atg gac agc cca gat ctg ggt acc			576																																																																																																																																																																										
Ala Ala Lys Phe Glu Arg Gln His Met Asp Ser Pro Asp Leu Gly Thr																																																																																																																																																																													
180	185	190																																																																																																																																																																											
gat gac gac gac aag atg gga gtg aaa gtt ctt ttt gcc ctt att tgt			624																																																																																																																																																																										
Asp Asp Asp Lys Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys																																																																																																																																																																													
195	200	205																																																																																																																																																																											
att gct gtg gcc gag gcc aaa cca act gaa aac aat gaa gat ttc aac			672																																																																																																																																																																										
Ile Ala Val Ala Glu Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn																																																																																																																																																																													
210	215	220																																																																																																																																																																											
att gta gct gta gct agc aac ttt gct aca acg gat ctc gat gct gac			720																																																																																																																																																																										
Ile Val Ala Val Ala Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp																																																																																																																																																																													
225	230	235	240																																																																																																																																																																										
cgt ggt aaa ttg ccc gga aaa aaa tta cca ctt gag gta ctc aaa gaa			768																																																																																																																																																																										
Arg Gly Lys Leu Pro Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu																																																																																																																																																																													
245	250	255																																																																																																																																																																											
atg gaa gcc aat gct agg aaa gct ggc tgc act agg gga tgt ctg ata			816																																																																																																																																																																										
Met Glu Ala Asn Ala Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile																																																																																																																																																																													
260	265	270																																																																																																																																																																											
tgc ctg tca cac atc aag tgt aca ccc aaa atg aag aag ttt atc cca			864																																																																																																																																																																										
Cys Leu Ser His Ile Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro																																																																																																																																																																													
275	280	285																																																																																																																																																																											
gga aga tgc cac acc tat gaa gga gac aaa gaa agt gca cag gga gga			912																																																																																																																																																																										
Gly Arg Cys His Thr Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly																																																																																																																																																																													
290	295	300																																																																																																																																																																											
ata gga gag gct att gtt gac att cct gaa att cct ggg ttt aag gat			960																																																																																																																																																																										
Ile Gly Glu Ala Ile Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp																																																																																																																																																																													
305	310	315	320																																																																																																																																																																										
ttg gaa ccc atg gaa caa ttc att gca caa gtt gac cta tgt gta gac			1008																																																																																																																																																																										
Leu Glu Pro Met Glu Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp																																																																																																																																																																													
325	330	335																																																																																																																																																																											
tgc aca act gga tgc ctc aaa ggt ctt gcc aat gtg caa tgt tct gat			1056																																																																																																																																																																										
Cys Thr Thr Gly Cys Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp																																																																																																																																																																													
340	345	350																																																																																																																																																																											
tta ctc aag aaa tgg ctg cca caa aga tgt gca act ttt gct agc aaa			1104																																																																																																																																																																										
Leu Leu Lys Lys Trp Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys																																																																																																																																																																													
355	360	365																																																																																																																																																																											
att caa ggc caa gtg gac aaa ata aag ggt gcc ggt ggt gat			1146																																																																																																																																																																										
Ile Gln Gly Gln Val Asp Lys Ile Lys Gly Ala Gly Gly Asp																																																																																																																																																																													
370	375	380																																																																																																																																																																											

<210> 22
<211> 382
<212> PRT
<213> Gaussia

<400> 22

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 20 25 30
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 35 40 45
 Gly Gln Thr Phe Trp Cys Asp His Ala Gly Ala Leu Leu Gly Asn Ser
 50 55 60
 Tyr Val Asp Asn Thr Ser Lys Val Thr Ala Asn Phe Val Lys Glu Thr
 65 70 75 80
 Ala Ser Pro Thr Ser Thr Tyr Asp Thr Tyr Val Glu Phe Gly Phe Ala
 85 90 95
 Ser Gly Ala Ala Thr Leu Lys Lys Gly Gln Phe Ile Thr Ile Gln Gly
 100 105 110
 Arg Ile Thr Lys Ser Asp Trp Ser Asn Tyr Thr Gln Thr Asn Asp Tyr
 115 120 125
 Ser Phe Asp Ala Ser Ser Ser Thr Pro Val Val Asn Pro Lys Val Thr
 130 135 140
 Gly Tyr Ile Gly Gly Ala Lys Val Leu Gly Thr Ala Pro Gly Ser Ala
 145 150 155 160
 Gly Leu Val Pro Arg Gly Ser Thr Ala Ile Gly Met Lys Glu Thr Ala
 165 170 175
 Ala Ala Lys Phe Glu Arg Gln His Met Asp Ser Pro Asp Leu Gly Thr
 180 185 190
 Asp Asp Asp Asp Lys Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys
 195 200 205
 Ile Ala Val Ala Glu Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn
 210 215 220
 Ile Val Ala Val Ala Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp
 225 230 235 240
 Arg Gly Lys Leu Pro Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu
 245 250 255
 Met Glu Ala Asn Ala Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile
 260 265 270
 Cys Leu Ser His Ile Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro
 275 280 285
 Gly Arg Cys His Thr Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly
 290 295 300
 Ile Gly Glu Ala Ile Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp
 305 310 315 320
 Leu Glu Pro Met Glu Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp
 325 330 335
 Cys Thr Thr Gly Cys Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp
 340 345 350
 Leu Leu Lys Lys Trp Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys
 355 360 365
 Ile Gln Gly Gln Val Asp Lys Ile Lys Gly Ala Gly Gly Asp
 370 375 380

<210> 23

<211> 864

<212> DNA

<213> Renilla reniformis

<220>

<221> CDS

<222> (61)...(762)

<223> GFP Clone-1

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 atg gat ctc gca aaa ctt ggt aag gaa gtg atg cct act aaa atc 108
 Met Asp Leu Ala Lys Leu Gly Leu Lys Glu Val Met Pro Thr Lys Ile
 1 5 10 15

aac tta gaa gga ctg gtt ggc gac cac gct ttc tca atg gaa gga gtt Asn Leu Glu Gly Leu Val Gly Asp His Ala Phe Ser Met Glu Gly Val 20 25 30	156
ggc gaa ggc aac ata ttg gaa gga act caa gag gtg aag ata tcg gta Gly Glu Gly Asn Ile Leu Glu Gly Thr Gln Glu Val Lys Ile Ser Val 35 40 45	204
aca aaa ggc gca cca ctc cca ttc gca ttt gat atc gta tct gtg gct Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val Ser Val Ala 50 55 60	252
ttt tca tat ggg aac aga gct tat acc ggt tac cca gaa gaa att tcc Phe Ser Tyr Gly Asn Arg Ala Tyr Thr Gly Tyr Pro Glu Glu Ile Ser 65 70 75 80	300
gac tac ttc ctc cag tcg ttt cca gaa ggc ttt act tac gag aga aac Asp Tyr Phe Leu Gln Ser Phe Pro Glu Gly Phe Thr Tyr Glu Arg Asn 85 90 95	348
att cgt tat caa gat gga gga act gca att gtt aaa tct gat ata agc Ile Arg Tyr Gln Asp Gly Gly Thr Ala Ile Val Lys Ser Asp Ile Ser 100 105 110	396
ttg gaa gat ggt aaa ttc ata gtg aat gta gac ttc aaa gcg aag gat Leu Glu Asp Gly Lys Phe Ile Val Asn Val Asp Phe Lys Ala Lys Asp 115 120 125	444
cta cgt cgc atg gga cca gtc atg cag caa gac atc gtg ggt atg cag Leu Arg Arg Met Gly Pro Val Met Gln Gln Asp Ile Val Gly Met Gln 130 135 140	492
cca tcg tat gag tca atg tac acc aat gtc act tca gtt ata ggg gaa Pro Ser Tyr Glu Ser Met Tyr Thr Asn Val Thr Ser Val Ile Gly Glu 145 150 155 160	540
tgt ata ata gca ttc aaa ctt caa act ggc aag cat ttc act tac cac Cys Ile Ile Ala Phe Lys Leu Gln Thr Gly Lys His Phe Thr Tyr His 165 170 175	588
atg agg aca gtt tac aaa tca aag aag cca gtg gaa act atg cca ttg Met Arg Thr Val Tyr Lys Ser Lys Lys Pro Val Glu Thr Met Pro Leu 180 185 190	636
tat cat ttc atc cag cat cgc ctc gtt aag acc aat gtg gac aca gcc Tyr His Phe Ile Gln His Arg Leu Val Lys Thr Asn Val Asp Thr Ala 195 200 205	684
agt ggt tac gtt gtg caa cac gag aca gca att gca gcg cat tct aca Ser Gly Tyr Val Val Gln His Glu Thr Ala Ile Ala Ala His Ser Thr 210 215 220	732
atc aaa aaa att gaa ggc tct tta cca tag atacctgtac acaattatttc Ile Lys Lys Ile Glu Gly Ser Leu Pro * 225 230	782
tatgcacgta gcattttttt ggaaatataa gtggatttgt tcaataaaaat attaaatata aaaaaaaaaaaaaa aaaaaaaaaaa aa	842 864

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	1	
gat ctc gca aaa ctt ggt ttg aag gaa gtg atg cct act aaa atc aac		107
Asp Leu Ala Lys Leu Gly Leu Lys Glu Val Met Pro Thr Lys Ile Asn		
5 10 15		
tta gaa gga ctg gtt ggc gac cac gct ttc tca atg gaa gga gtt ggc		155
Leu Glu Gly Leu Val Gly Asp His Ala Phe Ser Met Glu Gly Val Gly		
20 25 30		
gaa ggc aac ata ttg gaa gga act caa gag gtg aag ata tcg gta aca		203
Glu Gly Asn Ile Leu Glu Gly Thr Gln Glu Val Lys Ile Ser Val Thr		
35 40 45		
aaa ggc gca cca ctc cca ttc gca ttt gat atc gta tct gtt gct ttc		251
Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val Ser Val Ala Phe		
50 55 60 65		
tca tat ggg aac aga gct tat act ggt tac cca gaa gaa att tcc gac		299
Ser Tyr Gly Asn Arg Ala Tyr Thr Gly Tyr Pro Glu Glu Ile Ser Asp		
70 75 80		
tac ttc ctc cag tcg ttt cca gaa ggc ttt act tac gag aga aac att		347
Tyr Phe Leu Gln Ser Phe Pro Glu Gly Phe Thr Tyr Glu Arg Asn Ile		
85 90 95		
cgt tat caa gat gga gga act gca att gtt aaa tct gat ata agc ttg		395
Arg Tyr Gln Asp Gly Gly Thr Ala Ile Val Lys Ser Asp Ile Ser Leu		
100 105 110		
gaa gat ggt aaa ttc ata gtg aat gta gac ttc aaa gcg aag gat cta		443
Glu Asp Gly Lys Phe Ile Val Asn Val Asp Phe Lys Ala Lys Asp Leu		
115 120 125		
cgt cgc atg gga cca gtc atg cag caa gac atc gtg ggt atg cag cca		491
Arg Arg Met Gly Pro Val Met Gln Gln Asp Ile Val Gly Met Gln Pro		
130 135 140 145		
tcg tat gag tca atg tac acc aat gtc act tca gtt ata ggg gaa tgt		539
Ser Tyr Glu Ser Met Tyr Thr Asn Val Thr Ser Val Ile Gly Glu Cys		
150 155 160		
ata ata gca ttc aaa ctt caa act ggc aaa cat ttc act tac cac atg		587
Ile Ile Ala Phe Lys Leu Gln Thr Gly Lys His Phe Thr Tyr His Met		
165 170 175		
agg aca gtt tac aaa tca aag aag cca gtg gaa act atg cca ttg tat		635
Arg Thr Val Tyr Lys Ser Lys Lys Pro Val Glu Thr Met Pro Leu Tyr		
180 185 190		
cat ttc atc cag cat cgc ctc gtt aag acc aat gtg gac aca gcc agt		683
His Phe Ile Gln His Arg Leu Val Lys Thr Asn Val Asp Thr Ala Ser		
195 200 205		
ggt tac gtt gtg caa cac gag aca gca att gca gcg cat tct aca atc		731
Gly Tyr Val Val Gln His Glu Thr Ala Ile Ala Ala His Ser Thr Ile		
210 215 220 225		

aaa aaa att gaa ggc tct tta cca tag atatctatac acaatttttc 778
 Lys Lys Ile Glu Gly Ser Leu Pro *
 230

tatgcacgta gcattttttt ggaaatataa gtggattgt tcaataaaat attaaatata 838
 aaaaaaaaaa aaaaaaaaaa aa 860

<210> 25
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 <212> DNA
 <213> Renilla reniformis

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 <222> (61)...(762)
 <223> GFP Clone-3

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 atg gat ctc gca aaa ctt ggt ttg aag gaa gtg atg cct act aaa atc 108
 Met Asp Leu Ala Lys Leu Gly Leu Lys Glu Val Met Pro Thr Lys Ile
 1 5 10 15

aac tta gaa gga ctg gtt ggc gac cac gct ttc tca atg gaa gga gtt 156
 Asn Leu Glu Gly Leu Val Gly Asp His Ala Phe Ser Met Glu Gly Val
 20 25 30

ggc gaa ggc aac ata ttg gaa gga act caa gag gtg aag ata tcg gta 204
 Gly Glu Gly Asn Ile Leu Glu Gly Thr Gln Glu Val Lys Ile Ser Val
 35 40 45

aca aaa ggc gca cca ctc cca ttc gca ttt gat atc gta tct gtg gct 252
 Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val Ser Val Ala
 50 55 60

ttt tca tat ggg aac aga gct tat acc ggt tac cca gaa gaa att tcc 300
 Phe Ser Tyr Gly Asn Arg Ala Tyr Thr Gly Tyr Pro Glu Glu Ile Ser
 65 70 75 80

gac tac ttc ctc cag tcg ttt cca gaa ggc ttt act tac gag aga aac 348
 Asp Tyr Phe Leu Gln Ser Phe Pro Glu Gly Phe Thr Tyr Glu Arg Asn
 85 90 95

att cgt tat caa gat gga gga act gca att gtt aaa tct gat ata agc 396
 Ile Arg Tyr Gln Asp Gly Thr Ala Ile Val Lys Ser Asp Ile Ser
 100 105 110

ttg gaa gat ggt aaa ttc ata gtg aat gta gac ttc aaa gcg aag gat 444
 Leu Glu Asp Gly Lys Phe Ile Val Asn Val Asp Phe Lys Ala Lys Asp
 115 120 125

cta cgt cgc atg gga cca gtc atg cag caa gac atc gtg ggt atg cag 492
 Leu Arg Arg Met Gly Pro Val Met Gln Gln Asp Ile Val Gly Met Gln
 130 135 140

cca tcg tat gag tca atg tac acc aat gtc act tca gtt ata ggg gaa 540
 Pro Ser Tyr Glu Ser Met Tyr Thr Asn Val Thr Ser Val Ile Gly Glu
 145 150 155 160

tgt ata ata gca ttc aaa ctt caa act ggc aag cat ttc act tac cac 588
 Cys Ile Ile Ala Phe Lys Leu Gln Thr Gly Lys His Phe Thr Tyr His
 165 170 175

atg agg aca gtt tac aaa tca aag aag cca gtg gaa act atg cca ttg Met Arg Thr Val Tyr Lys Ser Lys Lys Pro Val Glu Thr Met Pro Leu 180 185 190	636
tat cat ttc atc cag cat cgc ctc gtt aag acc aat gtg gac aca gcc Tyr His Phe Ile Gln His Arg Leu Val Lys Thr Asn Val Asp Thr Ala 195 200 205	684
agt ggt tac gtt gtg caa cac gag aca gca att gca gcg cat tct aca Ser Gly Tyr Val Val Gln His Glu Thr Ala Ile Ala Ala His Ser Thr 210 215 220	732
atc aaa aaa att gaa ggc tct tta cca tag atacctgtac acaattatttc Ile Lys Lys Ile Glu Gly Ser Leu Pro * 225 230	782
tatgcacgta gcattttttt ggaaatataa gtggattgt tcaataaaat attaaatata tgtttgca aaaaaaaaaa aaaaaaaaaa a	842 873
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<211> 864	
<212> DNA	
<213> Renilla reniformis	
<220>	
<221> CDS	
<222> (61)...(759)	
<223> Human codon optimized Renilla reniformis GFP	
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aac ctg gag ggc ctg gtg ggc gac cac gcc ttc tcg atg gag ggc gtg Asn Leu Glu Gly Leu Val Gly Asp His Ala Phe Ser Met Glu Gly Val 20 25 30	156
ggc gag ggc aac atc ttg gag ggc acc cag gag gtg aag atc agc gtg Gly Glu Gly Asn Ile Leu Glu Gly Thr Gln Glu Val Lys Ile Ser Val 35 40 45	204
acc aag ggc gcc ccc ctg ccc ttc gcc ttc gac atc gtg agc gtg gcc Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val Ser Val Ala 50 55 60	252
ttc agc tac ggc aac cgg gcc tac acc ggc tac ccc gag gag atc agc Phe Ser Tyr Gly Asn Arg Ala Tyr Thr Gly Tyr Pro Glu Glu Ile Ser 65 70 75 80	300
gac tac ttc ctg cag agc ttc ccc gag ggc ttc acc tac gag cgg aac Asp Tyr Phe Leu Gln Ser Phe Pro Glu Gly Phe Thr Tyr Glu Arg Asn 85 90 95	348
atc cgg tac cag gac ggc acc gcc atc gtg aag agc gac atc agc Ile Arg Tyr Gln Asp Gly Gly Thr Ala Ile Val Lys Ser Asp Ile Ser 100 105 110	396
ctg gag gac ggc aag ttc atc gtg aac gtg gac ttc aag gcc aag gac Leu Glu Asp Gly Lys Phe Ile Val Asn Val Asp Phe Lys Ala Lys Asp 115 120 125	444
ctg cgg cgg atg ggc ccc gtg atg cag cag gac atc gtg ggc atg cag	492

Leu Arg Arg Met Gly Pro Val Met Gln Gln Asp Ile Val Gly Met Gln			
130	135	140	
ccc agc tac gag agc atg tac acc aac gtg acc agc gtg atc ggc gag			540
Pro Ser Tyr Glu Ser Met Tyr Thr Asn Val Thr Ser Val Ile Gly Glu			
145	150	155	160
tgc atc atc gcc ttc aag ctg cag acc ggc aag cac ttc acc tac cac			588
Cys Ile Ile Ala Phe Lys Leu Gln Thr Gly Lys His Phe Thr Tyr His			
165	170	175	
atg cggttaccgtg tac aag agc aag aag ccc gtg gag acc atg ccc ctg			636
Met Arg Thr Val Tyr Lys Ser Lys Lys Pro Val Glu Thr Met Pro Leu			
180	185	190	
tac cac ttc atc cag cac cgg ctg gtg aag acc aac gtg gac acc gcc			684
Tyr His Phe Ile Gln His Arg Leu Val Lys Thr Asn Val Asp Thr Ala			
195	200	205	
agc ggc tac gtg gtg cag cac gag aca gcc atc gcc gcc cac agc acc			732
Ser Gly Tyr Val Val Gln His Glu Thr Ala Ile Ala Ala His Ser Thr			
210	215	220	
atc aag aag atc gag ggc agc ctg ccc tagatacctg tacacaatta			779
Ile Lys Lys Ile Glu Gly Ser Leu Pro			
225	230		
ttctatgcac gtagcatttt ttggaaata taagtggtat tttcaataa aatattaaat			839
ataaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa			864
<210> 27			
<211> 233			
<212> PRT			
<213> Renilla reniformis			
<400> 27			
Met Asp Leu Ala Lys Leu Gly Leu Lys Glu Val Met Pro Thr Lys Ile			
1	5	10	15
Asn Leu Glu Gly Leu Val Gly Asp His Ala Phe Ser Met Glu Gly Val			
20	25	30	
Gly Glu Gly Asn Ile Leu Glu Gly Thr Gln Glu Val Lys Ile Ser Val			
35	40	45	
Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val Ser Val Ala			
50	55	60	
Phe Ser Tyr Gly Asn Arg Ala Tyr Thr Gly Tyr Pro Glu Glu Ile Ser			
65	70	75	80
Asp Tyr Phe Leu Gln Ser Phe Pro Glu Gly Phe Thr Tyr Glu Arg Asn			
85	90	95	
Ile Arg Tyr Gln Asp Gly Gly Thr Ala Ile Val Lys Ser Asp Ile Ser			
100	105	110	
Leu Glu Asp Gly Lys Phe Ile Val Asn Val Asp Phe Lys Ala Lys Asp			
115	120	125	
Leu Arg Arg Met Gly Pro Val Met Gln Gln Asp Ile Val Gly Met Gln			
130	135	140	
Pro Ser Tyr Glu Ser Met Tyr Thr Asn Val Thr Ser Val Ile Gly Glu			
145	150	155	160
Cys Ile Ile Ala Phe Lys Leu Gln Thr Gly Lys His Phe Thr Tyr His			
165	170	175	
Met Arg Thr Val Tyr Lys Ser Lys Lys Pro Val Glu Thr Met Pro Leu			
180	185	190	
Tyr His Phe Ile Gln His Arg Leu Val Lys Thr Asn Val Asp Thr Ala			
195	200	205	
Ser Gly Tyr Val Val Gln His Glu Thr Ala Ile Ala Ala His Ser Thr			
210	215	220	
Ile Lys Lys Ile Glu Gly Ser Leu Pro			

225

230

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<210> 28  
<211> 861  
<212> DNA  
<213> Pleuromamma
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<220>
<221> CDS
<222> (148) ... (741)
<223> *Pleuromamma luciferase*

<400> 28

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 tcgtcgaaag gtgatttctg tagtgatgtt tccttctggg atgtgatcaa gtacaaact
 gagagtcgac aatgctgtga cacaaaa atg ctt aga aat tgc gct agg aag caa
 Met Leu Arg Asn Cys Ala Arg Lys Gln
 1 5

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gag caa gtt tgc gcc gat gtg acc gag atg aaa tgc caa gca gtt gct 222
Glu Gln Val Cys Ala Asp Val Thr Glu Met Lys Cys Gln Ala Val Ala
   10          15          20          25

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tgg gcc gac tgt gga ccc aga ttt gat tcc act ggc agg aat aga tgc
Trp Ala Asp Cys Gly Pro Arg Phe Asp Ser Thr Gly Arg Asn Arg Cys
30 35 40

tac act gta ccg cac agg aag caa gtt cca gag tgc aaa caa gtc act
Tyr Thr Val Pro His Arg Lys Gln Val Pro Glu Cys Lys Gln Val Thr
60 65 70

aaa gat aac tgc gtt act gat tgg gaa gtt gac gcc aat ggc aac aag 414
Lys Asp Asn Cys Val Thr Asp Trp Glu Val Asp Ala Asn Gly Asn Lys
75 80 85

gtt tgg ggt ggt acc gag aaa tgc act cct gtc act tgg gaa gaa tgt
 Val Trp Gly Gly Thr Glu Lys Cys Thr Pro Val Thr Trp Glu Glu Cys
 90 95 100 105

```

aat atc gtg gag aaa gat gta gat ttt cca act gtc aag acg gaa tgc      510
Asn Ile Val Glu Lys Asp Val Asp Phe Pro Thr Val Lys Thr Glu Cys
           110          115          120

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ggc atc ctg tct cac ctt aag tat gca gac ttc ata gag gga cct tcc      558
Gly Ile Leu Ser His Leu Lys Tyr Ala Asp Phe Ile Glu Gly Pro Ser
          125           130           135

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cac tct ttg tct atg aga acc aat tgt cag gtc aag agt tca ttg gac      606
His Ser Leu Ser Met Arg Thr Asn Cys Gln Val Lys Ser Ser Leu Asp
    140           145           150

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tgc	cgg	cct	gtt	aag	acc	agg	aag	tgt	gca	acg	gtc	gag	tac	cac	gaa		654
Cys	Arg	Pro	Val	Lys	Thr	Arg	Lys	Cys	Ala	Thr	Val	Glu	Tyr	His	Glu		
155						160									165		

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tgc agc atg aag ccc caa gaa gac tgc agc cca gtc act gtt cat att      702
Cys Ser Met Lys Pro Gln Glu Asp Cys Ser Pro Val Thr Val His Ile
170           175           180           185
```

cct gac cag gag aaa gtt cac cag aag aag tgc ctc aca taaatqttat 751

Pro Asp Gln Glu Lys Val His Gln Lys Lys Cys Leu Thr
190 195

caattttagc tcttactaat ttaaacataa taaatatcac atcgaagccc tttattttat 811
agaagtgtaa tgcttgaata aatctagtga ataaaaaaaaaaaaaaa 861

<210> 29
<211> 198
<212> PRT
<213> Pleuromamma

<400> 29
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1 5 10 15
Thr Glu Met Lys Cys Gln Ala Val Ala Trp Ala Asp Cys Gly Pro Arg
20 25 30
Phe Asp Ser Thr Gly Arg Asn Arg Cys Gln Val Gln Tyr Lys Asp Tyr
35 40 45
Ala Tyr Lys Ser Cys Val Glu Val Asp Tyr Thr Val Pro His Arg Lys
50 55 60
Gln Val Pro Glu Cys Lys Gln Val Thr Lys Asp Asn Cys Val Thr Asp
65 70 75 80
Trp Glu Val Asp Ala Asn Gly Asn Lys Val Trp Gly Gly Thr Glu Lys
85 90 95
Cys Thr Pro Val Thr Trp Glu Glu Cys Asn Ile Val Glu Lys Asp Val
100 105 110
Asp Phe Pro Thr Val Lys Thr Glu Cys Gly Ile Leu Ser His Leu Lys
115 120 125
Tyr Ala Asp Phe Ile Glu Gly Pro Ser His Ser Leu Ser Met Arg Thr
130 135 140
Asn Cys Gln Val Lys Ser Ser Leu Asp Cys Arg Pro Val Lys Thr Arg
145 150 155 160
Lys Cys Ala Thr Val Glu Tyr His Glu Cys Ser Met Lys Pro Gln Glu
165 170 175
Asp Cys Ser Pro Val Thr Val His Ile Pro Asp Gln Glu Lys Val His
180 185 190
Gln Lys Lys Cys Leu Thr
195

<210> 30
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<212> DNA
<213> Ptilosarcus gurneyi

<220>
<221> CDS
<222> (34)...(747)
<223> Ptilosarcus Green Flourescent Protein

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Met Asn Arg Asn Val Leu Lys
1 5

aac act gga ctg aaa gag att atg tcg gca aaa gct agc gtt gaa gga 102
Asn Thr Gly Leu Lys Glu Ile Met Ser Ala Lys Ala Ser Val Glu Gly
10 15 20

atc gtg aac aat cac gtt ttt tcc atg gaa gga ttt gga aaa ggc aat 150
Ile Val Asn Asn His Val Phe Ser Met Glu Gly Phe Gly Lys Gly Asn
25 30 35

gta tta ttt gga aac caa ttg atg caa atc cgg gtt aca aag gga ggt 198
Val Leu Phe Gly Asn Gln Leu Met Gln Ile Arg Val Thr Lys Gly Gly
40 45 50 55

ccg ttg cca ttc gct ttc gat att gtt tcc ata gct ttc caa tac ggg Pro Leu Pro Phe Ala Phe Asp Ile Val Ser Ile Ala Phe Gln Tyr Gly 60 65 70	246
aat cgc act ttc acg aaa tac cca gac gac att gcg gac tac ttt gtt Asn Arg Thr Phe Thr Lys Tyr Pro Asp Asp Ile Ala Asp Tyr Phe Val 75 80 85	294
caa tca ttc ccg gct gga ttt ttc tac gaa aga aat cta cgc ttt gaa Gln Ser Phe Pro Ala Gly Phe Tyr Glu Arg Asn Leu Arg Phe Glu 90 95 100	342
gat ggc gcc att gtt gac att cgt tca gat ata agt tta gaa gat gat Asp Gly Ala Ile Val Asp Ile Arg Ser Asp Ile Ser Leu Glu Asp Asp 105 110 115	390
aag ttc cac tac aaa gtg gag tat aga ggc aac ggt ttc cct agt aac Lys Phe His Tyr Lys Val Glu Tyr Arg Gly Asn Gly Phe Pro Ser Asn 120 125 130 135	438
gga ccc gtg atg caa aaa gcc atc ctc ggc atg gag cca tcg ttt gag Gly Pro Val Met Gln Lys Ala Ile Leu Gly Met Glu Pro Ser Phe Glu 140 145 150	486
gtg gtc tac atg aac agc ggc gtt ctg gtg ggc gaa gta gat ctc gtt Val Val Tyr Met Asn Ser Gly Val Leu Val Gly Glu Val Asp Leu Val 155 160 165	534
tac aaa ctc gag tca ggg aac tat tac tcg tgc cac atg aaa acg ttt Tyr Lys Leu Glu Ser Gly Asn Tyr Tyr Ser Cys His Met Lys Thr Phe 170 175 180	582
tac aga tcc aaa ggt gga gtg aaa gaa ttc ccg gaa tat cac ttt atc Tyr Arg Ser Lys Gly Gly Val Lys Glu Phe Pro Glu Tyr His Phe Ile 185 190 195	630
cat cat cgt ctg gag aaa acc tac gtg gaa gaa gga agc ttc gtg gaa His His Arg Leu Glu Lys Thr Tyr Val Glu Gly Ser Phe Val Glu 200 205 210 215	678
caa cac gag acg gcc att gca caa ctg acc aca att gga aaa cct ctg Gln His Glu Thr Ala Ile Ala Gln Leu Thr Thr Ile Gly Lys Pro Leu 220 225 230	726
ggc tcc ctt cat gaa tgg gtg tagaaaatga ccaataact gggaaaccg Gly Ser Leu His Glu Trp Val 235	777
ataaccgttt ggaagcttgt gtataaaaaat tattttgggt cattttgtaa tgtgtatgtg tggtgtatga tcaatagacg tcgtcattca tagcttgaat ccttcagcaa aagaaacctc gaagcatatt gaaacctcga agcatattga aacctcgacg gagagcgtaa agagaccgca caaattaacg cgtttcaacc agcagttgga atctttaaac cgatcaaaac tattaatata aatatatata ccctgtataa ctttatataata tctatataagt ttgatattga ttaaatctgt tcttgatcaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa	837 897 957 1017 1077 1104

<210> 31
<211> 1279
<212> DNA
<213> Ptilosarcus gurneyi

<220>
<221> CDS
<222> (7)...(720)

<223> Ptilosarcus Green Flourescent Protein (GFP)

<400> 31
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 Met Asn Arg Asn Val Leu Lys Asn Thr Gly Leu Lys Glu Ile
 1 5 10

 atg tcg gca aaa gct agc gtt gaa gga atc gtg aac aat cac gtt ttt
 Met Ser Ala Lys Ala Ser Val Glu Gly Ile Val Asn Asn His Val Phe 96
 15 20 25 30

 tcc atg gaa gga ttt gga aaa ggc aat gta tta ttt gga aac caa ttg
 Ser Met Glu Gly Phe Gly Lys Gly Asn Val Leu Phe Gly Asn Gln Leu 144
 35 40 45

 atg caa atc cgg gtt aca aag gga ggt ccg ttg cca ttc gct ttc gac
 Met Gln Ile Arg Val Thr Lys Gly Gly Pro Leu Pro Phe Ala Phe Asp 192
 50 55 60

 att gtt tcc ata gct ttc caa tac ggg aat cgc act ttc acg aaa tac
 Ile Val Ser Ile Ala Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr 240
 65 70 75

 cca gac gac att gcg gac tac ttt gtt caa tca ttt ccg gct gga ttt
 Pro Asp Asp Ile Ala Asp Tyr Phe Val Gln Ser Phe Pro Ala Gly Phe 288
 80 85 90

 ttc tac gaa aga aat cta cgc ttt gaa gat ggc gcc att gtt gac att
 Phe Tyr Glu Arg Asn Leu Arg Phe Glu Asp Gly Ala Ile Val Asp Ile 336
 95 100 105 110

 cgt tca gat ata agt tta gaa gat gat aag ttc cac tac aaa gtg gag
 Arg Ser Asp Ile Ser Leu Glu Asp Asp Lys Phe His Tyr Lys Val Glu 384
 115 120 125

 tat aga ggc aac ggt ttc cct agt aac gga ccc gtg atg caa aaa gcc
 Tyr Arg Gly Asn Gly Phe Pro Ser Asn Gly Pro Val Met Gln Lys Ala 432
 130 135 140

 atc ctc ggc atg gag cca tcg ttt gag gtg gtc tac atg aac agc ggc
 Ile Leu Gly Met Glu Pro Ser Phe Glu Val Val Tyr Met Asn Ser Gly 480
 145 150 155

 gtt ctg gtg ggc gaa gta gat ctc gtt tac aaa ctc gag tca ggg aac
 Val Leu Val Gly Glu Val Asp Leu Val Tyr Lys Leu Glu Ser Gly Asn 528
 160 165 170

 tat tac tcg tgc cac atg aaa acg ttt tac aga tcc aaa ggt gga gtg
 Tyr Tyr Ser Cys His Met Lys Thr Phe Tyr Arg Ser Lys Gly Gly Val 576
 175 180 185 190

 aaa gaa ttc ccg gaa tat cac ttt atc cat cat cgt ctg gag aaa acc
 Lys Glu Phe Pro Glu Tyr His Phe Ile His His Arg Leu Glu Lys Thr 624
 195 200 205

 tac gtg gaa gaa gga agc ttc gtg gaa caa cac gag acg gcc att gca
 Tyr Val Glu Gly Ser Phe Val Glu Gln His Glu Thr Ala Ile Ala 672
 210 215 220

 caa ctg acc aca att gga aaa cct ctg ggc tcc ctt cat gaa tgg gtg
 Gln Leu Thr Thr Ile Gly Lys Pro Leu Gly Ser Leu His Glu Trp Val 720
 225 230 235

 tagaaaaatga ccaataact gggaaaaatc accaatatac tggggaaaaat gaccaattta
 ctggggaaaaa tgaccaatat actgttagaaa atcaccaata tactggggaa aatgaccaat 780
 840

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aaatactgtta gaaatgttca cactgggttg ataaccgtt	cgataaccgt ttgaaagctt	960
gtgtatacaa gttatttggg gtcattttgt aatgtgtatg	tgtgtgtat gatctataga	1020
cgtcgtcatt catacggtga atccctcagc	aaaagaaacc tcgaaggata ttgaaacctc	1080
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Ala Lys Ala Ser Val Glu Gly Ile Val Asn Asn His	Val Phe Ser Met	
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Glu Gly Phe Gly Lys Gly Asn Val Leu Phe Gly Asn	Gln Leu Met Gln	
35 40 45		
Ile Arg Val Thr Lys Gly Gly Pro Leu Pro Phe Ala	Phe Asp Ile Val	
50 55 60		
Ser Ile Ala Phe Gln Tyr Gly Asn Arg Thr Phe	Thr Lys Tyr Pro Asp	
65 70 75 80		
Asp Ile Ala Asp Tyr Phe Val Gln Ser Phe Pro Ala	Gly Phe Phe Tyr	
85 90 95		
Glu Arg Asn Leu Arg Phe Glu Asp Gly Ala Ile Val	Asp Ile Arg Ser	
100 105 110		
Asp Ile Ser Leu Glu Asp Asp Lys Phe His Tyr Lys	Val Glu Tyr Arg	
115 120 125		
Gly Asn Gly Phe Pro Ser Asn Gly Pro Val Met Gln	Lys Ala Ile Leu	
130 135 140		
Gly Met Glu Pro Ser Phe Glu Val Val Tyr Met Asn	Ser Gly Val Leu	
145 150 155 160		
Val Gly Glu Val Asp Leu Val Tyr Lys Leu Glu Ser	Gly Asn Tyr Tyr	
165 170 175		
Ser Cys His Met Lys Thr Phe Tyr Arg Ser Lys Gly	Gly Val Lys Glu	
180 185 190		
Phe Pro Glu Tyr His Phe Ile His His Arg Leu Glu	Lys Thr Tyr Val	
195 200 205		
Glu Glu Gly Ser Phe Val Glu Gln His Glu Thr Ala	Ile Ala Gln Leu	
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Gly Glu Gly Asn Ile Leu Glu Gly Thr Gln Glu Val	Lys Ile Ser Val	
35 40 45		
Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val	Ser Val Ala	
50 55 60		
Phe Ser Tyr Gly Asn Arg Ala Tyr Thr Gly Tyr Pro	Glu Glu Ile Ser	
65 70 75 80		
Asp Tyr Phe Leu Gln Ser Phe Pro Glu Gly Phe Thr	Tyr Glu Arg Asn	
85 90 95		
Ile Arg Tyr Gln Asp Gly Gly Thr Ala Ile Val Asp	Ser Asp Ile Ser	

100 105 110
Leu Glu Asp Gly Lys Phe Ile Val Asn Val Asp Phe Lys Ala **Asp** Asp
115 120 125
Leu Arg **Asp** Met Gly Pro Val Met Gln Gln Asp Ile Val Gly Met Gln
130 135 140
Pro Ser Tyr Glu Ser Met Tyr Thr Asn Val Thr Ser Val Ile Gly Glu
145 150 155 160
Cys Ile Ile Ala Phe Lys Leu Gln Thr Gly Lys **Asp** Phe Thr Tyr His
165 170 175
Met Arg Thr Val Tyr Lys Ser Lys Lys Pro Val Glu Thr Met Pro Leu
180 185 190
Tyr His Phe Ile Gln His **Asp** Leu Val Lys Thr Asn Val Asp Thr Ala
195 200 205
Ser Gly Tyr Val Val Gln His Glu Thr Ala Ile Ala Ala His Ser Thr
210 215 220
Ile **Asp** Lys Ile Glu Gly Ser Leu Pro
225 230